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   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                     Total number of hits satisfying chosen parameters:
                                                                             4390206 seqs, 2959870667 residues
                    nucleic search, using sw model
                                                       atgaccacacaaggcagatgg 21
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Gapop 10.0 , Gapext 1.0
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21
                                                                Scoring table:
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Perfect score:
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Add23578 Human sof Adm01725 Human CDN Ad124806 Intestina Acd93726 Human col Abx88992 Corn ear-Abx96477 Human pan Aax30910 Streptoco Add71720 Human uri Aaz96487 S. pneumo Add57025 Novel can Add57025 Novel can Add57025 Novel can Add57025 Novel wan Add57071 S. pneumon Adm91971 S. pneumon Adm91971 S. pneumon Adm91772 Human uri Adc5283 Human bea Ado07809 Human bol Add71722 Human bol Add71722 Human uri Adi26142 Human cDN Add24339 PRO polyp Add24339 PRO polyp Add24303 Human pro Add24675 Novel pro

ADQ57025 ABX07482 ADM91971 AASS5733 ACS5075 ADD71721 AACS9283 AACS1772 ADO07809

3 3

ADD71722 ADI26142 ADP24393 AAD32038

1446 1792 1792 1814 2354 2446 2488

AAX89852 AAF44675

ACD95453 ACD93726 ABX88992 ABV96477 AAX30910 ADD71720

21112 0110 01113 0113

## ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Searched:

Description

ADJ39000

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Query Match 1

Result No.

ABZ35798 ABX10041 ABL91763

ABV78191 ABZ35767 ABX10010 ABL91732

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:\*
geneseqn2003ds:\*
geneseqn2004as:\*
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geneseqn2002bs:\* geneseqn2002as:\*

geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\*

Geneseq 16Dec04:\* geneseqn1980s:\*

Database

geneseqn1990s:\*

SUMMARIES

Adj39000 SARS COro Abv78222 Human MMP Abx36094 Human MMP Abx10041 Human MMP Ab191763 Human MT4 Abx36191 Human MT4 Abx36191 Human MT4 Abx10010 Human MT4 Ab191732 Human MT4 Aa13389 Human MT4 Aa14351 Human MT4 Aa14351 Human MT4 Aa128234 Nucleotid Ade84832 Farnesyl Aaa14340 cDNA enco Abz20920 MT4-MMP c

Acf63409 Human MMP Adk14165 Human aut Ado28632 Human MMP Adq19326 Human sof

AAA13389 AAA14351 AAA12834 ADE84832 AAA1340 ABZ20920 AAA13377 ACF63409 ADC28632 ADO28632 ADO19326

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Estranged KNA molecules of 10-21 mucleotides than interference toward HCV in hepatitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified arrying HCV; (9) treating a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and colloube have antiinflammatory, hepatotropic and virucide activities. The modified RNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis D virus, hepatitis E virus, Ebbla virus, inammalian virus, rotavirus, recovirus, retrovirus, poliovirus, human papilloma virus, metapneumoniavirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring succeptibility to viral infections in patients. The present sequence represents the SARS coronavirus nucleotide sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA inhibition; daRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; gene; ds.
stranded RNA molecule of 10-30 nucleotides that inhibits replication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the target and having an overhang.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 12; Length 29751; 100.0%; Pred. No. 3.4; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                   is used in an example from the present invention.
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2001DE-01055280,
2001DE-01058411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-2002; 2002WO-EP000152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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The invention relates to inhibiting expression of a target gene (I) in  $\epsilon$  cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded

Claim 10; Page 176; 203pp; German.

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The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (GaRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (15, 82) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the distility (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary
structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into bathogenic for humans effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                         DB 6; Length 1560;
                                                                                                                                                                                                                                              Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                       Score 17.8; DB Pred. No. 87; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hadwiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MMP17 polynucleotide SEQ ID NO 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 73-74; 100pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                     1112 ATGACCÁCACGAGGCACATGG 1132
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                                                                                                                                                                                                      a gene related to the invention
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the target.
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RESULT 5

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(ds)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene alleast one oligoribonucleotide (dsRNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or spense expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with
                                                                                                                                                                                                                                                                                                                                                                                                         Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental; prion; inhibition; human; ds.
                                                                                         Gaps
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Local Similarity 90.5%; Score 17.8; DB 6; Length 1560;
Local Similarity 90.5%; Pred. No. 87;
hes 19; Conservative 0; Mismatches
                                                  Score 17.8; DB 6; Length 1560;
Pred. No. 87;
0; Mismatches 2; Indels 0
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               Sequence 1560 BP; 275 A; 549 C; 479 G; 257 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                    Human MMP17 DNA fragment SEQ ID 106.
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                                                                                                                            1 ATGACCACACAAGGCAGATGG 21
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Les 19; Conservative
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The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a singlestranded segment of 1-4 mt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or virusesy/rioxids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes the method provides more effective inhibition of gene expression than use
                                                                                                                                                   Human, HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting gene expression in cells, useful for e.g. treating tumors, introducing double-stranded complementary oligoRNA having unpaired
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Pred. No. 87;
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                                                                                                                     Human polynucleotide SEQ ID NO 106.
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ABL91763
ID <sup>®</sup> ABL91763 standard; DNA; 1560 BP.
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Matches 19, Conservative
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1112 ATGACCACACGAGGCACATGG 1132

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Query Match Best Loca Matches

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The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonucleotides (dsRNAI and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by lasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with
                                                                                                                                                                                                                                                                                                Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interferon. The present sequence is that of a target DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;
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90.5%; Pred. No. 89;
tive 0; Mismatches
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                            09-JAN-2001; 2001DE-01000588
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                                                                                                                                                                 Limmer S,
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                                                                                              (RIBO-) RIBOPHARMA AG
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es 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to inhibiting expression of a target gene (1) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (1) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytckine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into both in viro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hadwiger P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 153-154; 203pp; German.
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   virucide; protozoacide; gene; ds.
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target and having an overhang,
                                                                                                                                                                                                                                                                                                                                   09-JAN-2001; 2001DE-01000586.
26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
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                                                                         Homo sapiens
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Query Match Matches

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ABZ35767

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Gaps

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2; Indels

DB 6; Length 1818;

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gene at
(ds)
                                                                                                                                                                                   least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes, developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants) Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability, ABX09936-ABX1077 represent
                                                                                                     target gene by introducing into the cell that contains the target gen
least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds
structure of not more than 49 consecutive nucleotides (nt), where at
                                                                              This invention describes a novel method for inhibiting expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragments used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1818 BP; 310 A; 649 C; 571 G; 288 T; 0 U; 0 Other;
                             Disclosure, Page 55; 98pp; German
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84.8%; Score 17.8; DB 6; Length 1818; 90.5%; Pred. No. 89; Indels 5; Pred. No. 89; 0; Mismatches Local Similarity 90.5 Les 19; Conservative Query Match Best Loc Matches

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Gaps

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1370 ATGACCACACGAGGCACATGG 1390 1 ATGACCACACAGGCAGATGG 21 ద ò

ABL91732 standard; DNA; 1818 ABL91732 RESULT

(first entry) 28-MAY-2002 ABL91732; 

Human polynucleotide SEQ ID NO 75.

Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.

Homo sapiens

DE10100586-C1

11-APR-2002.

09-JAN-2001; 2001DE-01000586.

09-JAN-2001; 2001DE-01000586.

(RIBO-) RIBOPHARMA AG.

Rost S, Hadwiger P; Kreutzer R, Limmer S, WPI; 2002-270454/32. Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired

Claim 13; Page 53-54; 104pp; German.

terminal bases.

The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours

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This sequence represents the human matrix metalloprotease (MT4-MMP 2) nuclectide sequence. The invention relates to a mammalian transmembrane muclectide sequence. The invention relates to a mammalian transmembrane muclectide, its variants and the DNA sequences encoding them. Also included in the invention is a vector comprising the MMP DNA molecules, and cells transformed using the vector. The protein, DNA and antibodies directed against the polypeptide are useful in screening inhibitors and activators for use in treating are useful in screening inhibitors and activators for use in treating archivosis deformans, chronic rheumatoid arthritis, asthma, autoimmune diseases, atrophic dermatitis, psoriasis, contact dermatitis, hair loss, ischaemic diseases, immune reaction accompanying organ transplant, hepatitis, nephritis, pancreatitis, arteriosclerosis, leukaemia, malignant tumours, wounds, corneal ulcers, tissue damage or inflammation accompanying elekcoytic infiltration, together with brain disorders during cerebral apoplexia, Alzheimer's disease, dementia, multiple sclerosis, Parkinson's disease or brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matrix metalloproteame; MT4-MMP; treatment; arthrosis deformans; chronic rheumatoid arthritis; asthma; autoimmune disease; hepatitis; atrophic dermatitis; paoriasis; contact dermatitis; hair loss; nephritis; ischaemic disease; pancreatitis, arteriosclerosis; leukaemia; tumour; wound; corneal ulcer; tissue damage; inflammation; cerebral apoplexia; Alzheimer's disease; dementia; multiple sclerosis; Parkinson's disease;
but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physiologically-active transmembrane matrix metalloprotease polypeptide, useful in screening inhibitors and activators for treating e.g. arthrosis deformans, asthma and cancers.
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                                                                                                                                                                                               DB 6; Length 1818;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MT4-MMP matrixmetalloprotease nucleotide sequence.
                                                                                                                                                                                           Score 17.8; DE Pred. No. 89; 0; Mismatches
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Best Local Similarity 90.5%;
Matches 19; Conservative
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98JP-00291505
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29-SEP-1998;
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Sequence 2295 BP; 401 A; 807 C; 729 G; 358 T; 0 U; 0 Other;
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                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to antibodies against the novel murine and human transmembrane matrix metalloproceases MT4-MMP(2) (AAY90502 and AAY90503) and MT5-MMP (AAY90504 and AAY90505). The antibodies are useful for the diagnosis and screening of inhibitors and activators useful for treating or preventing a wide variety of medical conditions, such as arthrosis deformans, rheumatoid arthritis, asthma, autoimmune diseases and atopic diagnose and screen therapeutic or prophylactic agents for conditions affecting the brain, such as cerebral stroke and Alzheimer's disease. The antibodies of the invention may also be used for the prevention, and agnosis and treatment of psoriasis, contact dermatitis, hair loss, ischaemic diseases, immune reaction accompanying organ transplant, hairlish, pancreatitis, arteriosclerosis, leukaemia, malignant tumours, wounds, corneal ulcers, tissue damage or inflammation accompanying leukocytic infiltration, dementia, multiple sclerosis, Parkinson's disease or brain tumour. The present sequence represents a exemplification of the human MT4-MMP(2) gene used as a probe in an exemplification of the invention to screen a murine conn a purpose or prain to screen a murine conn a transplant or accompanying the invention to screen a murine conn accident.
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    tumours. The DNA can also be incorporated into a suitable vector for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody immunospecific for transmembrane matrix metalloprotease polypeptide, useful in screening of inhibitors and activators as drugs for, and for diagnosis of e.g. arthrosis deformans and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrix metalloprotease; MT4-MMP(2); transmembrane; human; antibody; drug screening; diagnosis; arthrosis deformans; rheumatoid arthritis; asthma; autolimune disease; artopic dermatitis; skin disorder; ischaemic disorder; arteriosclerosis; cancer; tissue damage; inflammatory disorder; neurological disorder; probe; ss.
                                                                                                                                             Gaps
                                                                                                                                         ö
                                                                                                    DB 3; Length 2295;
                                                             Sequence 2295 BP; 401 A; 807 C; 729 G; 358 T; 0 U; 0 Other;
                                                                                                                                         Indels
                                                                                                                                         5,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MT4-MMP(2) gene fragment, used as a probe.
                                                                                                                                         0; Mismatches
                                                                                                  Score 17.8;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 134-137; 152pp; Japanese.
                                                                                                                                                                                                                   1341 Argaccacacacacacarca 1361
                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                      AAA14351 standard; DNA; 2295 BP
                                                                                                                                                                                1 ATGACCACACAAGGCAGATGG
                                                                                                  84.8%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-JP005350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-00291501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-00291503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2000 (first entry)
                                                                                            Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furuya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-293115/25
                      in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200018805-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000
                                                                                                                                                                                                                                                                                                                                                             AAA14351;
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                                                                                                                                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth factor; protein inhibitor; proteame; damaged tissue; platelet-derived growth factor; PGF; platelet-derived growth factor; PGF; fibroblast growth factor; FGF; connective tissue derived growth factor; CGF; chrysalin; VGFF; keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF; transforming growth factor-beta; TGF-beta; matrix metalloproteiname; MMP; granulocyte macrophage colony stimulating factor; CM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PDGF), fibroblast growth factor (FGP), connective tissue derived growth factor (CTGP), connective tissue derived growth factor (GTGF), epidermal growth factor (KGF), vascular endothelial growth factor (WGF), and chrysalin. Inhibitors which are included in the composition of the invention include inhibitors of uncokinase-type plasminospen activator (UPA) and matrix metalloproteinase (MMP). The composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                                                     Gaps
                                                                  ö
   Length 2295;
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Occleston NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of matrix metalloproteinase-17.
   DB 3;
                                                                  0; Mismatches
Score 17.8;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcintosh FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 567; 572pp; English.
                                                                                                                                                                          1341 ATGACCACACGAGGCACATGG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "MMP-17"
                                                                                                                                    1 ATGACCACACAGGCAGATGG 21
                                                                                                                                                                                                                                                                                                                                                                          AAH28234 standard; cDNA; 2306 BP.
84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2000; 2000WO-IB001935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99GB-00030768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-2001 (first entry)
                                                                     19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies MJ, Huggins JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-418351/44.
P-PSDB; AAB84619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER LTD (PFIZ ) PFIZER INC
                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200149309-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH28234;
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor.
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Matrix metalloprotease, MT4-MMP(2); transmembrane; human; antibody; drug screening; diagnosis; arthrosis deformans; rheumatoid arthritis; asthma; autoimmune disease; atopic dermatitis; skin disorder;
                                                                                                                                                                                ischaemic disorder; arteriosclerosis; cancer; tissue damage, inflammatory disorder; neurological disorder; ss.
                                        AAA14340 standard; cDNA; 2423 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-293115/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanai N, Furuya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY90503.
                                                                                                                                                                                                                                                                                                                                WO200018805-A1.
                                                                                                                  cDNA encoding
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1998;
                                                                                           15-AUG-2000
                                                                                                                                                                                                                                                                                                                                                         06-APR-2000
                                                                 AAA14340;
                RESULT 14
AAA14340
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl-4-(3-chlorophenyl):1-methyl-2-(H)quinolinone, monitoring the therapy of a patient, treating a patient with Houkemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be
The present sequence encodes a human MMP-17, and is used to produce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                       Farnesyl transferase inhibitor modulated leukemia associated gene #51.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                ss; cytostatic; farnesyl transferase inhibitor; gene expression;
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%; Score 17.8; DB 10; Length 2306; 90.5%; Pred. No. 92; ive 0; Mismatches 2; Indels 0;
                                                              Score 17.8; DB 4; Length 2306;
Pred. No. 92;
0; Mismatches 2; Indels 0
                                      Sequence 2306 BP; 402 A; 810 C; 735 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2306 BP; 402 A; 810 C; 735 G; 359 T; 0 U; 0 Other;
                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 51; 346pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                  1344 ATGACCACACGAGGCACATGG 1364
                                                                                                                  1 ATGACCACACAGGCAGATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modulated in the presence of FTI.
                                                                                                                                                                                                           ADE84832 standard; DNA; 2306 BP
                                                                                                                                                                                                                                                                                                                               quinolinone; leukemia; cancer.
                                                             Match 84.8%;
Local Similarity 90.5%;
Les 19; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-2001; 2001US-0338997P.
30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-2002; 2002WO-US034784.
             composition of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2001; 2001US-0341012P
                                                                                                                                                                                                                                                            29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 90.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-513497/48.
                                                                                                                                                                                                                                                                                                                                                                                WO2003038129-A2.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raponi M;
                                                                                                                                                                                                                                    ADE84832;
                                                              Query Match
                                                                                        Matches
ន្តដូន
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/\*tag= a /product= "Human transmembrane matrix metalloprotease MT4 -MMP(2)"

99WO-JP005350.

98JP-00291501 98JP-00291503

Location/Qualifiers

.1917

human transmembrane matrix metalloprotease MT4-MMP(2).

(first entry)

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This sequence represents cDNA encoding a novel human transmembrane matrix metalloprotease MT4-MMP(2). MT4-MMP(2) has physiological activity different to that of MT4-MMP(2) the invention relates to antibodies against both murine and human MT4-MMP(2) the invention relates to antibodies against both murine and human MT4-MMP(2) for and AAY90503) and to antibodies against a novel murine and human transmembrane matrix metalloprotease MT5-MMP (AAY90504 and AAY90505). The antibodies are useful for the diagnosis and screening of inhibitors and activators of useful for treating or preventing a wide variety of medical conditions, continued a reflecting the anti-MT5-MMP antibodies may additionally be used to diagnose and screen therapeutic or prophylactic additionally be used to diagnose and screen therapeutic or prophylactic agents for conditions affecting the brain, such as cerebral stroke and Alzheimer's disease. The antibodies of the invention may also be used for the prevention, diagnosis and treatment of psoriasis, contact dermatitis, hair loss, ischaemic diseases, immune reaction accompanying organ transplant, hepatitis, nephritis, pancreatis, arteriosclerosis, inflammation accompanying lenkocytic infiltration, dementia, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Antibody immunospecific for transmembrane matrix metalloprotease polypeptide, useful in screening of inhibitors and activators as drugs for, and for diagnosis of e.g. arthrosis deformans and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.8; DB 3; Length 2423; Pred. No. 93; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2423 BP; 404 A; 871 C; 794 G; 354 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sclerosis, Parkinson's disease or brain tumour
                                                                                                                                                                                                Example 2; Page 102-108; 152pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%;
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Best Local Similarity 90.5
Matches 19; Conservative
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Gaps

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1344 ATGACCACACGAGGCACATGG 1364

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1 ATGACCACACAAGGCAGATGG

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The present invention relates to a monoclonal antibody which binds specifically to the MT4-MMP (membrane type-matrix metalloproteinase) scatalytic domain. The antibody is applicable in diagnosis and remedies for MT4-MMP participated diseases e.g. inflammations and cancer particularly rheumatoid arthritis. The present sequence is a human coding sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                       MT4-MMP; catalytic domain; antibody; inflammation; cancer; gene; membrane type-matrix metalloproteinase; antiinflammatory; antirheumatoid; antiarthritic; rheumatoid arthritis; cytostatic; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody specifically binding to natural or solubilized MT4-MMP, applicable in diagnosis and remedies for MT4-MMP participated diseases e.g. inflammations and cancer particularly rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

84.8%; Score 17.8; DB 8; Length 2423;
Best Local Similarity 90.5%; Pred. No. 93;
Matches 19; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2423 BP; 404 A; 871 C; 794 G; 354 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     MT4-MMP catalytic domain antibody related coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miki I, Ohta S, Shitara K, Furuya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 50-54; 63pp; Japanese.
                        1469 ATGACCACGAGGCACATGG 1489
 1 ATGACCACACAAGGCAGATGG 21
                                                                                                                             ABZ20920 standard; cDNA; 2423 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-2002; 2002WO-JP005788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2001; 2001JP-00176256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-148808/14.
P-PSDB; AAO19713.
                                                                                                                                                                                                                                                                                                                                                                                     WO2002101046-A1.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                   26-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2002.
                                                                                                                                                                 ABZ20920
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0; Gaps

Search completed: May 15, 2005, 11:25:18 Job time : 17.1953 sec8

1469 ATGACCACGAGGCACATGG 1489

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1 ATGACCACACAGGCAGATGG 21

Appl Appl Appl

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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Sequence 1, Application US/09810671

Patent No. 6455291

GENERAL INFORMATION:

ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/810,671

CURRENT APPLICATION NOWER: 2001-06-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 745., Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
CURRENT APPLICANTON NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 7452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381752H1
US-09-313-294A-7452
US-09-949-016-91184
US-09-949-016-201853
US-08-416-588-39
US-08-471-504A-39
US-08-486-756A-39
US-08-486-756A-39
US-08-487-077A-39-39
US-08-487-077A-39-39
US-09-178-115-39
US-09-178-115-39
US-09-178-115-39
US-09-178-115-39
US-09-178-115-39
US-09-178-116-39
US-09-178-1173
US-09-68-68-78-30
US-09-949-016-5564
US-09-949-016-5564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TGACCACACAGGCAGATGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 TGTCCACACAAGGCTGATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 90.0 ies 18; Conservative
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    TYPE: DNA
ORGANISM: Human
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LENGTH: 2354
  RESULT 2
US-09-810-671-1
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Sequence 1, Appli
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Sequence 30, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 12871, A
Sequence 12871, A
Sequence 12871, A
Sequence 12614, A
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Sequence 169668,
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Sequence 11, Appl
Sequence 11, Appl
                                                                                                                                                May 15, 2005, 11:11:51 ; Search time 4.6102 Seconds (without alignments) 7453.434 Million cell updates/sec
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Sequence 1, Appli
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Sequence 18, Appl
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Sequence 1641, A
Sequence 15314, A
Sequence 15390, A
Sequence 12805, A
Sequence 14060, A
Sequence 992, App
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    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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    /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-016-000-9

US-09-816-527-30

US-10-109-854-3

US-10-339-656-3

US-09-949-016-12871

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US-09-513-999C-993
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 1, Application US/10109854

Sequence 1, Application US/10109854

Sequence 1, Application US/10109854

Sequence 1, Application US/10109854

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: 100109,854

TITLE OF INVENTION: 1002-04-01

PRIOR APPLICATION NUMBER: 00/227,470

PRIOR APPLICATION NUMBER: 09/810,671

PRIOR APPLICATION NUMBER: 09/810,671

PRIOR PELING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LINTH: 2354
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APPLICANT: YAN, Chunhua et al.

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/10/339,656

CURRENT FILING DATE: 2003-01-10

PRIOR PLICATION NUMBER: 09/810,671

PRIOR PAPLICATION NUMBER: 09/810,671

PRIOR APPLICATION NUMBER: 60/227,470

PRIOR APPLICATION NUMBER: 60/227,470

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PRACESEQ FOR Windows Version 4.0

SEQ ID NO 1

LENGTH: 2354
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                                      Query Match 80.0%; Score 16.8; DB 3; Length 2354; Best Local Similarity 90.0%; Pred. No. 1e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0;
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Patent No. 6733978
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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; ORGANISM: Homo sapien
US-10-109-854-1
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US-10-339-656-1
US-09-810-671-1
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                         APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: ARCADIOM, Ingrid E.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
TITLE OF INVENTION: PROTEIN KINASE MOLECULES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ingvre C.
STRRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FRALSED for Windows Version 2.0 CURRENT APPLICATION DATA:
FILLING PARTION NUMBER: US/09/016 000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0465 US
TELECOMUNICATION INFORMATION:
TELECHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-961-527-30/c
; Sequence 30, Application US/08961527
Patent No. 6420135
; GENERAL INFORMATION:
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; Sequence 9, Application US/09016000
; Patent No. 5962232
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ilarity 90.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650-855-05
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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Sequence 3, Application US/10109854

Patent No. 6630371

GENERAL INFORMATION: 66303371

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THRREOF

TITLE OF INVENTION: THRREOF

FILE REFERENCE: CLOO0758DIV

CURRENT FAPLICATION NUMBER: 08/10/109,854

CURRENT FILING DATE: 2002-04-01

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 21234
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Patent No. 6733978
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) ORGANISM: Homo sapien
US-10-339-656-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
US-10-109-854-3
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-810-671-3

Sequence 3, Application US/09810671

Patent No. 645291

GENERAL INFORMATION:

APPLICANT: YAN Chunhua et al

TITLE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/810,671

CURRENT APPLICATION NUMBER: US/09/810,671

NUMBER OF SEQ ID NOS: 5
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9769;
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                                                            ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectre 486,33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 3;
Pred. No. 1.3e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 21234
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,333
REFERENCE/DOCKET NUMBER: PB340PI
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 9769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3808 rcaccaacaacaaccacrrcc 3789
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Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-961-527-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human
US-09-810-671-3
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GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILLE REFERENCE: CLOOO758DIV2
CURRENT APPLICATION NUMBER: US/10/339,656
CURRENT APPLICATION NUMBER: 10/109,854
PRIOR APPLICATION NUMBER: 10/109,854
PRIOR APPLICATION NUMBER: 09/810,671
PRIOR APPLICATION NUMBER: 60/227,470
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 5
SOFWARE: FastSEQ for Windows Version 4.0
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                                                   Gaps
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    Length 21234;
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Ouery Match

80.0%; Score 16.8; DB 4;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 16.8; DB 4;
90.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 2;
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8.09-949-016-12871/c
; Sequence 12871, Application US/09949016
; Patent No. 6812339
                                                                                                                                             8379 TGACCACATCAGGCAGATGG 8398
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8379 rgaccacarcagecagarge 8398

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Query Match
Best Local Similarity
Matches 18; Conserv
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US-09-949-016-15947
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Sequence 17063, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEC ID NOS: 207012
SOFTHARE: FREESEQ FOR WINDOWS VETRION 4.0
SEQ ID NO 17063
LENGTH: 100837
JULIANT: VENTER, J. Craig et al.

JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEAGE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12871

LENGTH: 100836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 80.0%; Score 16.8; DB 4; Length 100836; Local Similarity 90.0%; Pred. No. 1.7e+02; hes 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

80.0%; Score 16.8; DB 4; Length 100837;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1).T.(100836)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1) ... (100837)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TGACCACACAGGCAGATGG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
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Best Local S
Matches 18
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Sequence 15947/C

Sequence 1547, Application US/09949016

Sequence 1547, Application US/09949016

Patent NO. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOR 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PELLING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASLESQ for Windows Version 4.0

SEQ ID NO 15947

LENGTHEN DATE: DA
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GENERAL INCRAMATION:
TITLE OF INVENTEN, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12614
TENAME. ASSOCIATION
TITLE OF INVENTION WINDOWS VERSION 4.0
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90.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 2;
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; Sequence 12614, Application US/09949016
; Patent No. 6812339
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12614
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Best Local Similarity 90.0°
Matches 18; Conservative
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RESULT 14 US-09-949-016-16061/c

RESULT 12

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Sequence 16061, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUMBER OF SEG OF Windows Version 4.0
SEQ ID NO 16661
LENGTH: 250958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOCTWARE: FREISEQ FOR Windows Version 4.0
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 16.8; DB 4; Length 250958; 90.0%; Pred. No. 1.9e+02; tive 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-099-949-016-169568/c
; Sequence 169568, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)...(250558)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGACCACACAAGGCAGATG 20
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Matches 18; Conservative
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US-09-949-016-169568
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ORGANISM: Human
FEATURE:
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Search completed: May 15, 2005, 14:23:03 Job time : 8.6102 secs

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Sequence 9, Appli Sequence 3, Appli Sequence 16, Appl Sequence 15, Appl

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Sequence 1 Sequence 2 Sequence 7 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1

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US-10-901-417-50 US-10-425-114-26875

US-10-406-209-4 US-10-480-464-5

ALIGNMENTS

Sequence Sequence Sequence

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Squence 2, Application US/10764075;
Squence 2, Application US/10764075;
Publication No. US20040265796A1
GENERAL INFORMATION:
APPLICANT: Brises, Thomas
APPLICANT: Lipkin, Ian W.
APPLICANT: Lipkin, Ian W.
TITLE OF INVENTION: Methods and Kits for Detecting SARS-Associated Coronavirus
FILE REFERENCE: 5199-87
CURRENT APPLICATION NUMBER: US/10/764,075;
CURRENT APPLICATION NUMBER: DO04-01-23
FRIOR APPLICATION NUMBER: Provisional Application 60/463,704
PRIOR FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 16
SSOCIATE PATENT OF SEQ ID NOS: 16
SSOCIATE PAT
US-10-827-757-1

US-10-899-447-8

US-10-899-947-8

US-10-899-947-9

US-10-899-947-9

US-10-899-95-3

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ive 0; Mismatches 0;
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ORGANISM: artificial sequence
          Best Local Similarity 100.
Matches 21; Conservative
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Sequence 11
Sequence 3,
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Sequence 4
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                                                                                                                                                                                                                               May 15, 2005, 12:53:36 ; Search time 15.5004 Seconds
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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US-10-699-936-11

US-10-699-936-11

Sequence 11, Application US/10699936

Sequence 11, Application Wo. US2005009582A1

GENERAL INFORMATION:

APPLICANT: Gillin-Ross, Laura

APPLICANT: Scholl, David R.

APPLICANT: Scholl, David R.

APPLICANT: Workworth, David E.

APPLICANT: Workworth, David E.

APPLICANT: Workworth, David E.

APPLICANT: Scholl, David E.

APPLICANT: Scholl, David R.

TITLE OF INVENTION: Syndrome Coronavirus

FILE REFERENCE: DHI-07986

CURRENT APPLICATION NUMBER: US/10/699,936

CURRENT FILING DATE: 2003-11-03

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.2

SEQ ID NO 11

FERRENT FOR APPLICATION OF SEQ ID NOS: 87

SEQ ID NO 11

FERRENT FOR APPLICATION OF SEQ ID NOS: 87

SEQ ID NO 11
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, Joseph D.
TITLE OF INVENTION: Syndrome Coronavirus
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT APPLICATION NUMBER: US/10/699,936
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
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Sequence 3, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION:
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT PILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
PRIOR FILING DATE: 2003-07-12
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Pred. No. 1.4;
; Mismatches 0;
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; ORGANISM: SARS coronavirus Shanhgai LY
US-10-699-936-11
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Best Local Similarity 100.0%; Pr
Matches 21; Conservative 0;
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US-10-699-936-7
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Best Local Similarity 100..
Best 21; Conservative
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APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                         APPLICANT: Briese, Thomas
APPLICANT: Lipkin, Ian W.
APPLICANT: Lipkin, Ian W.
APPLICANT: Palacios, Gustavo
APPLICANT: Dabado, Omar
TILE OF INVENTION: Methods and Kits for Detecting SARS-Associated Coronavirus
FILE REFERENCE: 5199-84
CURRENT APPLICATION NUMBER: US/10/764,075
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: Provisional Application 60/463,704
PRIOR PILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 1
LENGTH: 1136
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US-10-699-936-16
; Sequence 16, Application US/10699936
; Publication No. US20050095582A1
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                                                                                                                                                                                              Sequence 1, Application US/10764075; Publication No. US20040265796A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: artificial sequence
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ORGANISM: SARS-COV ZJ-HZ01
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Best Local Similarity 100.
Matches 21; Conservative
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US-10-699-936-7
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                     Length 28920;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10889447

Publication No. US20050075307A1

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: MOULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR FILING DATE: 2003-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
TITLE REFERENCE: RTS-068502
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: PRESSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                  0; Indels
                                                                                                                                     DB 19;
1.6;
                                                                                                                                   Query Match
100.0%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 21; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 29291
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                            ; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: n is any nucleotide US-10-889-447-4
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Publication No. US20050075307A1
GENERAL INFORMATION:
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APPLICANT: Jain, R
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; Sequence 6, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
   APPLICANT: Jain, Ravi
   TILE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
   TILE REFERENCE: RTS-0685US
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2003-07-12
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SEQ ID NO 6
; SEQ ID NO 6
; LENGTH: 28920
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Publication No. US20050075307A1
GENERAL INFORMATION:
TGENERAL THORMATION:
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
TITLE REFERENCE: RTS-0685U6;
FULE REFERENCE: RTS-0685U6;
FULE REPETION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12;
PRIOR FILING DATE: 2004-07-12;
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                  Score 21; DB 19; Length 24774; Pred. No. 1.6;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                 TYPE: DNA ORGANISM: SARS CORONAVIRUS isolate BJ01
                                                                                                                                 NAME/KEY: misc_feature
i. LOCATION:
i. OTHER INFORMATION: n is any nucleotide
US-10-889-447-3
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  SEQ ID NO 3
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LENGTH: 28920
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US-10-889-447-6
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                                                                                  APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODILATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR PILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FRASER for Windows Version 4.0
SEQ ID NO 8
LENGTH: 29727
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Sequence 17, Application US/10839729
Eublication No. US20050002953A1
GENERAL INFORMATION:
APPLICANT: Jens Herold
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
FILE REFERENCE: BIORANK: 013A
CURRENT APPLICATION NUMBER: US/10/839,729
PRIOR APPLICATION NUMBER: 60/468703
PRIOR PILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21; DB 19;
Pred. No. 1.6;
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Sequence 8, Application US/10889447 Publication No. US20050075307A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: SARS coronavirus Urbani
US-10-889-447-8
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; ORGANISM: SARS coronavirus Urbani
US-10-699-936-1
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US-10-839-729-17
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                                    DB 19; Length 29430;
1.6;
                                                                                                                                                                                                                                                                                                                       ## Sequence 15, Application US/10839729

| Sequence 15, Application US/10839729
| Publication No. USZO05002953A1
| Publication No. USZO05002953A1
| GENERAL INFORMATION:
| APPLICANT: Jens Herold
| TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
| TITLE OF INVENTION: AND METHODS OF USE
| FILE REPRENCE: BIODRANK. 013A
| CURRENT RILING DATE: 2004-05-04
| PRIOR APPLICATION NUMBER: US/10/839,729
| PRIOR APPLICATION NUMBER: 05/468703
| PRIOR FILING DATE: 2003-05-06
| NUMBER OF SEQ ID NOS: 49
| SQCTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 15
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                              Ouery Match 100.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 21; Conservative 0; Mismatches
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Best Local Similarity
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US-10-827-757-1
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US-10-889-447-8
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; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-17

Query Match
Best Local Similarity 100.0%; Score 21; DB 18; Length 29736;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 1 ATGACCACAAGGCAGATGG 21

Db 29383 ATGACCACAAGGCAGATGG 29403

Search completed: May 15, 2005, 16:48:44
Job time: 16:5004 secs
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CO664875 592 bp mRNA linear EST 23-JUL-2004
DG40-174112 DG40-uterus Canis familiaris cDNA 3', mRNA sequence.
CO664875
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K-EST0092
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PUDEP40TD
PUHSM35TB
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AGENCOURT
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HS 2016 A
mm48c01.x
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ILS-GN024
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MR0-BN018
AV975852
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 592)
Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
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                       BF347731
BG251251
BQ680344
BW167886
BX955716
BC045610
BE627254
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AQ244968
BM822423
CC631183
CC001155
CC392087
AX036023
AQ666653
BE010668
AV975852
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Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION bloschence AG
Waldhoferetrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
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87.6%; Score 18.4; DB 7;
Best Local Similarity 95.0%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 1;
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9615"
/tissue type="uterus"
dev_stage="adut"
/lab_host="plil08"
/clone_lib="DG40-uterus"
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BX440072
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AQ221669
A1426376
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Canis familiaris
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LOCUS
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SOURCE
ORGANISM
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BF032477/c
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CO664875/c
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AQ663120 HS 5364 A
AQ133467 HS 53039 A
AQ80134 HS 5037 B
R17506 yg02e12.r1
B1536734 396079 MA
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CF894618 1247-6411.
BJ200351 BJ200351
CN833628 Ha mx0_15
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8645.536 Million cell updates/sec
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                                                                                                                                                  May 15, 2005, 11:03:36 ; Search time 92.4581 Seconds
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                                                   nucleic search, using sw model
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/mol type="mRNA" Coping State | Mol type="mRNA" 
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ISB1-43B21_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-43B21,
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/clone lib="1SB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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Washington University School of Medicine
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Xenopus tropicalis
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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
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Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTACTATAGGG
Class: BAC ends
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapber@mmail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMSSES row: j column: 19
High quality sequence start: 23
High quality sequence stop: 182.
Location/Qualifiers
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1 (Dases 1 to 772)
NIH-MGC http://mgc.nci.nih.gov/.
NiH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 1578)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
     601452977F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856626 5',
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Tissue Procurement: ATC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Matches 19; Conservative
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Gaps ; GSS 05-JAN-2004

DB 9; Length 1139;

Best Loc Matches

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JOURNAL

TITLE

FEATURES

ORIGIN

ACCESSION VERSION KEYWORDS

DEFINITION

RESULT 5 CN924279

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AL119881

DKFZp761M2224 rl 761 (synonym: hamy2) Homo sapiens cDNA clone
DKFZp761M2224-5', mRNA sequence.
                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1466
High quality sequence stops: 249 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1466 Std Error: 0.00
Seq primer: MISRP1
High quality sequence stop: 249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dkfz-heidelberg.de,
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 356)

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Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="GDB:396062"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:23715"
/sex="female"
                         The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 ATGACCACACGAGGCACATGG 232
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Genome Project.
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Best Local Similarity
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      Wilson, R
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                                                                                                                                                                                                                         CN924279 295 bp mRNA linear EST 07-JUN-2004 000414AELA009380HT (AELA) Royal Gala young expanding leaf Malus x domestica cDNA clone AELA009380, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Rosales; Rosaceae; Maloideae; Malus.

(bases 1 to 295)

Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y. HortResearch Apple EST Project

Unpublished (2004)
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 329)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaekis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Abbert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db xref="taxon:3750"
/clone="AELA009380"
/dev=stage="Young, expanding"
/dev=stage="Young, expanding"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"
                           Gaps
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y095D0:r1 Soares infant brain 1NDB Homo sapiens CDNA clone IMAGE:23715 5' similar to SP:COG2 MOUSE P33434 72 KD TYPE IV COLLAGENASE PRECURSOR; mRNA sequence.
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84.8%; Score 17.8; DB 7; Length 295;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels
                       Indels
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Pred. No. 9.5e+02;
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1. 295
/organism="Malus x domestica"
                                                                                                                                                                                                                                                                                                                                                         Malus x domestica (cultivated apple)
Malus x domestica
                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@hortresearch.co.nz.
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                                                                                               323 ATGACCACACAAGGCAGA 340
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100.08;
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T77190.1 GI:694393
                       18; Conservative
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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Gaps

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ880134 486 bp DNA linear GSS 09-NOV-1999
HS_5037_B1_A04_T7 RPCI-11 Human Male BAC Library Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ133467
HS_3039_A2_E05_MR_CIT_Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=10 Row=I, genomic survey
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe1.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                          Gaps
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 309 row: I column: 10
                                                                                                                                                                                                        Length 456;
                                                                                                                                                                                                                                                                      Indels
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/db_xref="taxon:9606"
/clone="Plate=3039 Col=10 Row=I"
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6
                                                                                                                                                                                                 84.8%; Score 17.8; DB 8; ilarity 90.5%; Pred. No. 1.1e+03; Conservative 0; Mismatches 2.
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/organism="Homo sapiens"
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Location/Qualifiers
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Matches 19; Conserv
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Eax: (206) 616-3887
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plates 940 row: I column: 3
Seg primer: T7
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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/clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
      No sl sequence available.
This clone (DKPZp761M2224) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                        /tissue_type='amygdala"
/dev_stage="adult"
/lab_host="bH10B"
/clone lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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84.8%; Score 17.8; DB 1; Length 356;
Best Local Similarity 90.5%; Pred. No. 1e+03;
Matches 19; Conservative 0; Mismatches 2; Indels
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/db_xref="taxon:9606"
/clone="Plate=940 Col=3 Row=I"
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Location/Qualifiers
                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp761M2224"
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AQ669320.1 GI:5202066
GSS.
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and

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Unpublished (1995)
Conteact: Wilson RK
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1446
High quality sequence stops: 332
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; Contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1446 Std Exror: 0.00
Seq primer: MI3RP1
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Grasse, R., Wary, J.B., White, J., Cho, J., Fhrenkrug, S.C., Bennett, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Guackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
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1 Similarity 90.5%; Pred. No. 1.1e+03;
19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 332.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="GDB:403197"
/db_xref="taxon:9606"
/clone="IMAGE:30850"
                                                                                       The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
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Bos taurus
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BI536734/c
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 8805 row: B column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 486)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 bp mRNA linear EST 14-APR-1995
yg05012.rl Soares infant brain lNIB Homo sapiens cDNA clone
IMAGE:30850 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 506)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
genomic clone Plate=8805 Col=7 Row=B, genomic survey sequence.
AQ880134
                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/db_xref="taxon:9606"
/clone="Plate=8805 Col=7 Row=B"
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Location/Qualifiers
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Homo sapiens (human)
Homo sapiens
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Homo sapiens
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R17506.1 GI:771116
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les 19; Conservative
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                                                                                                                                                                                                                                                                     Hood, L.
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Enkaryota, Metazoa Chordata, Craniata, Vertebrata; Euteleostomi; Eukaryota; Metazoa Chordata, Sciurognathi; Muridae, Murinae, Mus. Eukaryota; Metazoa Chordata, Sciurognathi; Muridae, Murinae, Mus. 1 (Dases 1 to 547)

1 (Dases 1 to 547)

2 Tidwell, R., Cliffton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I., Tsagareishvili, R., Belaygorod, L., Grow, A., Maguire, L., Waterston, R. and Wilson, R., Washi Good and Mike Lovett Gontact: Jeff Gordon and Mike Lovett Washi, Human Genetics Division Medicine Washington University School of Medicine Washington University School of Medicine Sakary Drimers. The final DONA was amplified by PCR using modified SMART primers. The final DONA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in pAMPI vector in annealing reaction with Uracil DNA was cloned in partice by X.Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI.
                                                                                                                                                                                                                                                                                                               CF804618
1ad76d11.yl Gastric Epithelial Progenitor 2 Mus musculus cDNA 5' similar to SW:ROAL BOVIN P09867 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="adult"
/lab_host="DHSalpha"
/clone lib='Gastric Epithelial Progenitor 2"
/clone lib='Gastric Epithelial Progenitor 2"
/note="Vector: pAMPI; lst strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in pAMPI vector in annealing reaction with Uracil DNA Glycosylase (UDG). Library constructed by T. Korshunova and M. Lovett. Library materials provided by Mills JC & Gordon JI."
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/db_xref="taxon:10090"
/tissue_type="Laser-captured isthmal cells from tox176
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                                            Length 543;
                                            84.8%; Score 17.8; DB 9; 90.5%; Pred. No. 1.1e+03;
                                                                                             0; Mismatches
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/organism="Mus musculus"
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Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                             367 ATGTCCACATAAGGCAGATGG 387
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               USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRimers
FORWARD: AGGARACAGCTATCACAT
BACKWARD: GTTTTCCCAGTCACACAT
COLUMN: 2
Seq primer: ATTTAGGTGACCATAGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
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Canis familiaris
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 543)
1 (bases 1 to 543)
8 (krichesses, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
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/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="Wactor: pGNV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog_Library"
/note="Site_1: BetXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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/organism="Canis familiaris"
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CE836567
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Contact: Smith TPL
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Contact: Jadasu Shiri-1

Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-6856
Fax: 81-685
            EST 21-OCT-2003
                                                                                                                                                                                                                                                                           Physicomitrella patens subsp. patens
Physicomitrella patens subsp. patens
Physicomitrella patens subsp. patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta;
Eryopsida; Funariidae; Funariales; Funariaceae; Physicomitrella.
1 (bases I to 558)
Nishiyama, T., Kamiya, T., Shin-i, T., Seki, M., Nishide, H.,
Uchiyama, T., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Kohara, Y. and Hasebe, M.
Comparative genomics of Physicomitrella patens gametophytic
transcriptome and Arabidopsis thallana: Implication for land plant
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/mol_type="mkNA"
/mol_type="mkNA"
/mol_type="mkNA"
/clone="pphnago1"
/tissue_type="mixture of chloronemata, caulonemata and rhizoid-like proconemata"
/clone_lib="mormalized full length cDNA library,
chloronemata, caulonemata and rhizoid-like protonemata"
BJ200351 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physocomitrella patens subsp. patens cDNA clone pphn3g23 5', mRNA sequence.
BJ200351.1 GI:18368266
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1 (Seess 1 to 1873)
Lim, P.L., Kurup, A., Gopalakrishna, G., Chan, K.P., Wong, C.W., Ng, L.C., Se-Thoe, S.Y., Oon, L., Bai, X., Stanton, L.W., Ruan, Y., Miller, L.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B. and Leo, Y.S.
Laboratory-acquired severe acute respiratory syndrome (SARS) - Singapore 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1873)
Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
               Gaps
AY394978
AY394979
AY394982
AY559086
AY559082
AY394983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="SARS coronavirus Sin0409"
/mol_type="genomic RNA"
/db xref="taxon:26647"
/country="Singapore"
                                                                                                                                                                                                                                                         AYS34758S4 1873 bp RNA
SARS coronavirus Sin0409, partial sequence.
AYS34761
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SARS coronavirus Sin_WNV
SM SARS coronavirus Sin_WNV
Viruses; SRRMA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
E 1 (bases 1 to 1938)
S Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W.,
Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y.,
Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J.,
Ang,B. and Leo,Y.S.
Laboratory-acquired severe acute respiratory syndrome (SARS) -
Singapore 2003
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P 2 (Nases 1 to 1938)
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Wei, C.L., Lee, C., Lin, S., Thoreau, H., Vega, V.B., Stanton, L.W.
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/organism="SARS coronavirus Sin_WNV"
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            A1334/62S6 1938 bp RNA
SARS coronavirus Sin_WNV, partial sequence.
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	TCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACCACCTTCGGG  [[][][][][][][][][][][][][][][][][]		961 TTGTGCAGAATGAATTCTCGTAACTAACAGCACAAGTAGGTTTAGTTAACTTTAATCTC  1692 TTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTAATCTC  1021 ACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCACTTT  1752 ACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCACATTT  1752 ACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCACATTT  1081 TCATCGAGGCCACGCGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGC 1136  111	AY290752 SARS coronavirus ZJ01 isolate ZJ01b uncharacterized protein uncharacterized protein 7a, uncharacterized protein 7b, uncharacterized protein 7b, uncharacterized protein 8b, uncharacterized protein 8b, uncharacterized protein 8b, uncharacterized protein 9b, and uncharacterized protein 9b, and AY290752	AY290752.2 GI:38735509 SARS coronavirus ZJO1 SARS coronavirus ZJO1 Viruses; seRNA positive-strand viruses, no DNA stage; Nidcoronavirus.  1 (bases 1 to 2810) Li,L., Wang,Z., Lu,Y., Bao,Q., Chen,S., Wu,N., Cheng,S., Izhang,Y., Yan,J., Mei,L., Wang,X., Zhu,H., Yu,Y., Zhang,M Yao,J., Lu,Q., Yao,P., Bo,X., Wo,J., Wang,S. and Hu,S. Severe acute repliratory syndrome-associated coronavirus sand its characterization	Chin. Med. J. 116 (9), 1288-1292 (2003) 22889812 14527350 2 (bases 1 to 2810) Wang, Z.G., Li, L.J., Luo, Y., Zhang, J.Y., Wang, M.Y., Cheng, S.Y. Zhang, Y.J., Wang, X.M., Lu, Y.Y., Wu, N.P., Mei, L.L. and Wang, Z.Mong, Y.J., Wang, X.M., Lu, Y.Y., Wu, N.P., Mei, L.L. and Wang, Z.Mongecular biological malysis of genotyping and phylogeny of acute respiratory syndrome associated coronavirus Chin. Med. J. 117 (1), 42-48 (2004)

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SARS coronavirus SZ13
SARS coronavirus SZ13
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales
Coronaviridae; Coronavirus.

1 (bases 1 to 8581)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
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                                      2254 CAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAAACATTCCCACCAACAACAGAGCC
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Guan, Y. and Zheng, B.J.
Direct Submitssion
Submitted (26-MAY-2003) Microbiology, The University of Hong
University Pathology Building, Queen Mary Hospital, Pokfulam
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation and characterization of viruses related to the coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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iive 0; Mismatches
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AY304487
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Matches 1136; Conservative
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Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
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Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.P., Yuen, K.Y., Peirie, J.S.M. and
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ISDEVARDLSLQFKRPINPTDQSSYIVDSVAVKNGALHPYFDKAGQKTYERHPLSHFV **GDSTEVSVKMFDAYVDTFSATFSVPMEKLKALVATAHSELAKGVALDGVLSTFVSAAR** QGVVDTDVDTKDVI ECLKLSHHSDLEVTGDSCYNFMLTYNKVENMTPRDLGACI DCNA

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REFERENCE 2 (bases 1 to 29350) AUTHORS CONSTIM The Saks epidemiology consortium of Guangdong TITLE JOURNAL Submitted (19-SEP-2003) Guangdong, China FEATURES 1. 29350 /organiam="Saks coronavirus LC2" /mol type="genomic RNA" /isolate="Lc2" /db_xref="taxon:249084"	Query Match Best Local Similarity 100.0%; Score 1136; DB 14; Length 29350; Best Local Similarity 100.0%; Pred. No. 0; Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 AGGCATCGTATGGGTTGCAACTGAGGAGCCTTGAATACACCCAAAGACCAATTGGCAC 60	28105 AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCAC	Qy         61         CCGCAATGCTAATAACAATGCTGCCACCGTGCTACAACATTCCTCAAGGAACAACATTGCC 120           Db         28165         CCGCAATCCTAATAACAATGCTGCCACCGTGCTTCCTCCAAGGAACAACAATTGCC 28224	OY 121 AAAAGGCTTCTACGCAGAGGAAGCAGCAGCAGTCAAGCCTCTTCTCGCTCCTCATC 180	OY 181 ACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCACTAGGGGAAATTCTCCTGC 240	Oy 241 TCGAATGGCTAGGCGAGGTGGAAACTGCCCTCGGCCTATTGCTGCTAGACAGATTGAA 300	Qy 301 CCAGGTTGAGAGAAAGTTTCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTCACTAA 360	OY 361 GAAATCTGCTGAGGCATCTAAAAGCCTCGCCAAAAAGGTACTGCCACAAAACGTA 420	OY 421 CAACGTCAAGGATTTGGGAACGTGGTCCAGAACAACAAGGAAATTTCGGGGA 480	Qy         481         CCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCCACAATTTGC         540           Db         28585         CCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCCAATTTGC         28644		Oy 601 AACATCGCTGACTTATCATGGATTGGATGACAAAGATCCACAATTCAAAGA 660 	661 CAACGTCATACTGCTGAACAAGGCACATTGACGCATACAAAACATTCCCACCAACAGAGCCC	Db 28765 CAACGTCATACTGCTGAACAAGCACATTGACGCATACAAACATTCCCACCAACAGGCC 28824  Oy 721 TAAAAAGGACAAAAAGAAAAAGCTGATGAAGCTCAGCCTTTGCCGCAGAGAAAAAAAA	Db 28825 TAAAAAGACAAAAAGAAAAAGACTGATGAGCTCTGCCGCAGAGACAAAAGAA 28884 Ov 781 GCAGCCCACTGTCTTCCTGCGGCTGACATGAATGATTTCTCCAGACAACTACA 840	

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TITLE From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus JOURNAL Unpublished EPERENCE 2 (bases 1 to 29350)  REFERENCE 2 (bases 1 to 29350)  AUTHORS CONSTM The SARS epidemiology consortium of Guangdong TITLE Direct Submission JOURNAL Submitted (19-SEP-2003) Guangdong, China Location/Qualifiers  FEATURES 1. 29350  // Organism-"SARS coronavirus LC4" // Mol Lype="genomic RNA" // isolate="LC4" // isolate="LC4" // isolate="LC4" // isolate="LC4" // isolate="LC4"	ORIGIN  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 1136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 AGGCATCGARGGGTGCAACTGAGGAGCCTTGAATACACCCAAAGACCACATTGACA 60  28105 AGGCATCGTATGGTTGCAACTGAGGAGCCTTGAATACACACAC	121 AAAAGCCTTCTACGCAGAGGAAAGCAGAGCCGCAGTCAAGCCTCTTCTCGCTCCTCTT	361 GARATCTGCTGCTGAGGCATCTAANAAGCCTCGCCAAAAACGTACTGCCACAAAACGTA  [	DD 28645 TCCAAGTGCTTGCATTGGAATGTCACGCATTGGCAAGGAGTCAACCTTGGGG 28704  Qy 601 AACATGGCTGACTTATCATGGAGCCATTAAATTGGATGAAGATCCACAATTCAAGA 660  LINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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NNI PRELICAATRQVTNVITTRI SLKGGKIVSTCFKLMLKATLLCVLAALVCYI VMPV
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PVVAAI ITREI GFIV PWGLAGFYLLARINGDFLHFLPRVFSAVWNI CYTPSKLIEVSDFA
TSACVLAAECTI FFADMGKPVPFCYDTNLLEGSI SYSBLRPDTRYVLANGSI IG QFBYT
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( Passes 1 to 29573)

Chang, J. Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.
SARS coronavirus TC2, clinical specimen
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Chang,J., Lin,T., Chen,C., Lin,T., Chan,W. and Shih,M.
Chang,J., Lin,T., Chen,C., Lin,T., Chan,W. and Shih,M.
Direct Submission
Submitted (09-JUL-2003) Department of Molecular Medicine, China
Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung 404, Taiwan Amino acid sequence updated by submitter
                                                                                                                                                                                                                                                                                             TCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGC 1136
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3 (bases 1 to 29573)
Chang, Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                               AGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATTGGCAC
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Best Local Similarity 100.
Matches 1136; Conservative
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FKLNIKLLGIGGKPCIKVATVQSKMSDVKCTSVVLLSVLQQLAVESSSKLMAQCVQLH
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CDS

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codon start=1 .13344

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MYTKHGSGALRELTRELNGANYTRYNDNFOCEDDEOYELLOI.TOFLARARGKSMCTIASEQ
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PVSYKLDGVTYTE I EPKLDGYY FPADDLNQMTGFTKPASRELSVT	100.0%; Score 1136; DB 14; Length 29573; milarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 AGGCATCGTATGGGTTGCAACTGAGGGGGCCTTGAATACACCCCAAAGACCACATTGGCAC 60	CGGGAATCCTAATAACAATGCTGCCACGGTGCTACAACTTCCTCAAGGAACAACATTGCC 120	GGCAATCCTAATAACAATGCTGCCACGGTGCTACAACTTCCTCAAGGAACAACATTGCC 28556	AAAAGGCTTCTACGCAGAGGGAAGCAGAGGGGGCAGTCAAGCCTCTTCTCGCTCCTCATC 180	ACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGC 240	300	TCGAATGGCTAGCGGAGGTGGAACTGCCTCGCGCTATTGCTGCTAGACAGATTGAA 28736	CCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAAGGCCAAACTGTCACTAA 360 	GADATCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAACAGTA 420		480	ANCGICACI CANGCATTI ISASABANGI GGI CCAGAACAAACCCAAGAAATTI CGGGGGA CAACACCAAAAACAAAAAAAAAAAAAAAAAA	CCANGERT AND AGRACIANT TACAMACH TO TO THE CONTROL OF THE CONTROL O	TCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCAAGGTCACACCTTCGGG 600	CCAAGTGCCTCTGCATTTTTTTTGGAATGTCACGCATTGGCATGGAAGTCACACTTCGGG 29036	AACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGA 660		CARGICATACTIGATGAGGAGATTGAGGGATAGAAAAATTCCAGGAGGGGC 720 	Taaaaaggacaaaaagaaaaagactgatgagctcagcctttgccgcagagacaaaagaa 29216		GCAGCCCACTGTGACTCTTCCTGCGGCTGACATGGATTTCTCCCAGACAACTTCA 29276	900		ACAAGGCAATGGGTTATTTAAACTTTTGCGATTCGGTTAACATAATGTGCTGCTG 960 ACAAGGCAGATGGGGTATGTAAACGTTTTGCGAATTCCGTTTACGATAGTAGTCTACTC 29396	TTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTAATCTC 1020
	imi ;	AGGCATCGTAT											י נ	CCANGACCIAN              CCAAGACCIAN	TCCAAGTGCCT	TCCAAGTGCCT			CAACGICATAC		GCAGCCCACTG	gcagcccacre	AAATTCCATGA	AAATTCCATGA	ACAAGGCAGAT 	TTGTGCAGAAT
	Query Match Best Local Si Matches 1136;	Oy 1 Db 28437	0, 61	28	Oy 121 Db 28557	Oy 181		Db 28677	Oy 301 Db 28737	Oy 361	Db 28797	•	<b>3</b>	Uy 481 Db 28917	Oy 541	Db 28977	(	29	Qy 661 Db 29097	Db 29157		Db 29217		8	Qy 901 Db 29337	Qy 961

29456	1080	29516		2	
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 aggcatcgtatgggttgcaa.....tgaataatgctagggagagc 1136 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 4390206 seqs, 2959870667 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Abz16240 Arabidops Abq21011 Oligonuc1 Abq21010 Oligonuc1 Ach231062 Cotton an Aaf93473 cDNA enco Abq30524 Oligonuc1 Aa878289 DNA encod Aa878289 DNA encod Ab133547 Human imm AbX31470 Signal tr Ab13547 Human imm Abx31470 Signal tr Ab170565 Chemical1 Aa861384 Human gen Acc45236 Human gen Acc45236 Human ner Aba177168 Human ner Aba177168 Human ner Aba177199 DNA fragm Acn43984 Mouee gen Ad889773 Oligonuc1 Abn80136 Human che Aba21125 Human che Aba812739 DNA fragm Acn43984 Mouee gen Ad889773 Oligonuc1 Abn80136 Human GEN Abn80136 Human GEN Abn80136 Human GEN Abn80136 Human GEN
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## ALIGNMENTS

small interfering RNA, siRNA, modified ribonucleotide, viral replication inhibition, hepatitis C virus, HCV, hepatitis C; antiinflammatory, hepatotropic, virucide, hepatitis A virus, hepatitis B virus, Ebola virus, influenza virus, rotavirus, reovirus, retrovirus, poliovirus, human papilloma virus, metapneumoniavirus, coronavirus, viral infection, gene, ds. SARS coronavirus nucleotide sequence. ADJ39000 standard; DNA; 29751 BP. (first entry) 06-MAY-2004 ADJ39000; RESULT 1 ADJ39000 

SARS coronavirus.

WO2004011647-A1.

05-FEB-2004.

25-JUL-2003; 2003WO-US023104

26-JUL-2002; 2002US-0398605P

(CHIR ) CHIRON CORP.

Houghton M; Seo MY, Han J,

WPI; 2004-143862/14.

New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.

Example 10; Fig 3; 74pp; English.

The present invention describes a small interfering RNA (siRNA) which comprises a modified ribonucleotide, where the siRNA is resistant to RNase and retains the ability to inhibit viral replication. Also described: (1) inactivating a virus in a parient; (2) making a modified siRNA that targets a nucleic acid sequence in a virus; (3) a double-

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Rice gene,
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stranded RNA molecule of 10-30 nucleotides that inhibits replication of hepaticis C virus (HCV); (4) inhibiting resplication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule, (7) a host cell comprising a DNA segment encoding the RNA molecule, (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepaticis of n subject; (10) a modified siRNA molecule comprising a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target of norleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand, (11) inducing targeted RNA interference in a patient. The modified siRNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for inactivating virus, hepatitis A virus, hepatitis D virus, hepatitis E virus, EDOIa virus, influenza virus, metapneumoniavirus or cornect or compensate for cellular physiological subortion can be used to correct or compensate for cellular physiological cannoniatis and/or alleviate symptoms of a viral infections in patients. The present sequence represents the SARS coronavirus nucleotide sequence,
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CAACGTCATACTGCTGAACAAGAAGAATGACGCATACAAAAACATTCCCACCAACAACAGAGGCC
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                                                TAAAAAGGACAAAAAAAAAAAACACTGATGAAGCTCAGCCTTTGCCCGCAGAGAAAAAA
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Xie Z,
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Whitham S,
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F, Quan S,
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mouse; ds; POZ; poxvirus and zinc finger domain, transgenic; schizophrenia; POZ disruption; neuroleptic; 129/OlaHsd; C57BL/6; cognitive abnormality; decreased PPI response; prepulse inhibition; weight:tyce abnormality; decreased body weight; decreased organ weight; decreased organ weight;

Mouse POZ domain disruption construct, 3' arm targeting sequence

(first entry)

20-FEB-2003

ABX14055;

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expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is seful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 CTCAAGGAACAACATTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGGGGCGCAGTCAAG 161
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useful

gene

New transgenic mouse comprising a disruption in a POZ domain gene, as a model for disease and for identifying agents that modulate gen expression and function, which are potential agents for treating

29-MAR-2001; 2001US-0280372P 24-SEP-2001; 2001US-0324590P 29-MAR-2002; 2002WO-US009714

WO200279422-A2

Mus sp. Synthetic.

Mus

10-OCT-2002.

(DELT-) DELTAGEN INC

WPI; 2003-067440/06.

Suenther C;

Example 1, Fig 3; 68pp; English.

schizophrenia.

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The invention relates to a transgenic mouse comprising a disruption in a novel poxvirus and zinc finger (POZ) domain gene, where there is no native expression of the POZ domain gene, where there is no native expression of the POZ domain gene. The disrupted gene is created in 129/0laH6d mouse embryonic stem cells. The mice are then bred with C57BL/6 female mice to create the FI generation. The PL homozygous crangenic mouse compared to wild type includes a cognitive abnormality shown by a decreased prepulse inhibition (PPI) response to a startle response test. The transgenic mouse can also show weight-type chown lites such as decreased body weight, decreased organ weights chosen, liver, kidney, thymus and heart), decreased organ weights (e.g. spleen, liver, kidney, thymus and heart-to-body weight ratios). The transgenic mouse is useful as a model for disease and weight ratios (e.g. spleen, liver, kidney, thymus and heart-to-body weight ratios). The transgenic mouse is useful as a model for disease and confidential agents for treating schizophrenia. The present sequence represents the sequence on the 3' arm of the disruption construct which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 8;
Pred. No. 0.043;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               targets the POZ domain gene
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RESULT 4 ABL33863/c RESULT

ABX14055 standard; DNA; 200 BP.

RESULT 3 ABX14055

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20-FEB-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, profilessy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             689 GACGCATACAAAACATTCCCACCAACAGGCCTAAAAAGGACAAAAAGAAAAAGACTGAT 748
                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiartestelocic; antianaemic; cytostatic; notoropic; neuroprotective; anti-HIV; anticonvulant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthmatic; artidiosese; arteriosclerosis; anamicior; ancer; eye disease; arteriosclerosis; anamic, acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             629 AAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 41.8; DB 6; Length 7359; 55.0%; Pred. No. 0.28; tive 0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1836; 32pp + Sequence Listing; German
                                                                          Human immune system associated gene SEQ ID NO: 1836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1218 TAATTTTACCATCAAACGAATTATCAAAA 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              749 GAAGCTCAGCCTTTGCCGCAGAGACAAA 777
 ВР
ABL33863 standard; DNA; 7359
                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP007537
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01-SEP-2000; 2000DE-01043826.
                                                 (first entry)
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Best Local Similarity 55.0
Matches 82; Conservative
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                                                                                                                                                                                                                                        WO200200928-A2
                                                                                                                                                                                                                Homo sapiens.
                                                 26-MAR-2002
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                        ABL33863
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ABX14053 standard; DNA; 463

ABX14053

ABX14053

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The invention relates to a transgenic mouse comprising a disruption in a novel poxvirus and zinc finger (POZ) domain gene, where there is no native expression of the POZ domain gene. The disrupted gene is created in 129/OlaHsd mouse embryonic stem cells. The mice are then bred with C57BL/6 female mice to create the FI generation. The F2 homozygous cutants are created by crossbreeding the F1 mice. The phenotype of the transgenic mouse compared to wild type includes a cognitive abnormality shown by a decreased prepulse inhibition (PPI) response to a startle response test. The transgenic mouse can also show weight type of the crossed brown and expensed by thymus and heart), decreased organ weights (e.g. spleen, liver, kidney, thymus and heart), decreased organ-to-body weight ratios (e.g. spleen, liver, kidney, thymus and heart-to-body weight ratios). The transgenic mouse is useful as a model for disease and for identifying agents that modulate gene expression and function, which are potential agents for treating schizophrenia. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic mouse comprising a disruption in a POZ domain gene, useful as a model for disease and for identifying agents that modulate gene expression and function, which are potential agents for treating
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                                       mouse; ds, gene; POZ; poxvirus and zinc finger domain; transgenic; schizophrenia; POZ disruption; neuroleptic; 129/OlaHsd; C57BL/6; cognitive abnormality; decreased PPI response; prepulse inhibition; weight-type abnormality; decreased body weight; decreased organ weight;
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Mouse poxvirus and zinc finger (POZ) domain gene.
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2001; 2001US-0280372P.
24-SEP-2001; 2001US-0324590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DELT-) DELTAGEN INC
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                                                                                                                                                                                                                                                                                                                                                    WO200279422-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             schizophrenia.
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Oligonucleotide for detecting cytosine methylation SEQ ID NO 30203

(first entry)

12-JUL-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined similtaneously. ABG13410-
                                                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 AAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATT 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 AAAAAAACCAAAAAAAACGCACAAAATAAATAAAAGGCAATAAAAAGGCACACAAAAAAA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              689 GACGCATACAAAACATTCCCACCAACAGGGCCTAAAAAGGACAAAAAGAAAAAAGACT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 30204.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                                                                                                     01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disclosure of the invention
 (first entry)
                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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                                                                                                                                                              WO200218632-A2.
                                                                                                                                   Homo sapiens
12-JUL-2002
                                                                                                                                                                                            07-MAR-2002
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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

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Guetig

Berlin K,

Piepenbrock C,

Olek A,

WPI; 2002-371829/40.

(EPIG-) EPIGENOMICS AG.

01-SEP-2001; 2001WO-EP010074. 01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543.

WO200218632-A2 Homo sapiens

07-MAR-2002.

Claim 12; 56pp + Sequence Listing; 56pp; German.

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomacleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP'8); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation of states of the methylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 AAATTGGATGACAAAGACCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATT 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    689 GACGCATACAAAACATTCCCACCAACAGGGCCTAAAAAAGGACAAAAAGAAAAAGT 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK31241 standard; DNA; 9830 BP.
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ABK31241/c RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in prepare transduction associated genes. The DNA sequences are chemically adjust transduction associated genes. The DNA sequences are chemically acidised using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligomucleotides and/or PNA oligomers for detecting the cytosine methylation state (DGS islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, transduction embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK11158-ABK311545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 AAACATTCCCAACCAACAGGCCTAAAAAGGACAAAAAGAAAAAGAAAAAGAAAAAGACTGAGCTCAGC 758
                                                                                                                                                                                                           Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to chemically modified DNA sequences of
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                                                                                                                                              Signal transduction associated gene modified complementary DNA #42.
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Pred. No. 2;
0; Mismatches 78; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-EP007472.
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2000DE-01043826.
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Local Similarity 52.4%;
nes 86; Conservative
                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200200926-A2
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01-SEP-2000;
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                                                                     23-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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ABK31241;
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The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is constraint of provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for cetecting cytosine methylations, as well as a method which is considered by the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The considerably modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACA
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                                                                                                      Chemically treated cell signalling DNA sequence complementary to#43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with cell signaling e.g. cancer, comprises chemica sequences of genes associated with cell signaling.
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ABL70196 standard; DNA; 9830 BP.
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01-SEP-2000; 2000DE-01043826
                                                                      (first entry)
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                                                                                                                                                              ds.
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                                                                                                                                        Cell signalling; cyt
tumour; cytostatic;
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                                                                                                                                                                                                                                  WO200202807-A2.
                                                                                                                                                                                                Unidentified.
                                                                     01-JUL-2002
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                                   ABL70196;
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RESULT 10

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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, cigomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and hylation patterns of such geness, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, as sequence data for this
                                                                                                                                                                                                  Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; sesphageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification and is associated with the human gene regulation associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                         Human gene regulation-associated gene oligonucleotide #109.
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                     ВЪ.
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07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01035259.
01-SEP-2000; 2000DE-01043826.
                     AAS61154 standard; DNA; 9830
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                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-017470/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177375-A2
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                           29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001
                                                                AAS61154;
AAS61154/
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) compered seasociated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the chetylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                    Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostetic; anticonvulent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                 Human chemically modified disease associated gene SEQ ID NO 80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.5%; Score 39.2; DB 6; Length 9830; 52.4%; Pred. No. 2;
                                                                             78; Indels
                                                        CTTTGCCGCAGAGAAAAAAAGAAGCAGCCCACTGTGACTCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 80; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĸ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                                                                                    ABN80063 standard; DNA; 9830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
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Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200200927-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                            15-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                        759
                                                                                                                                                                                                                         ABN80063;
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639 ACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACA 6121 ACACCAAAACGAAAAACCAAAATATCCACATCCGACAAAAAAACCCACGTACCTAAATA 699 AAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAAGACTGATGAAGCTCAGC

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CACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCC

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
ACAAAGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.4%; Score 39; DB 5; Length 481;
Best Local Similarity 49.3%; Pred. No. 0.54;
Matches 99; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                  6001 chaaaaccrcccaaaaaarcaaaccraccacaahrachchicch 5958
                                                                                                                                               CTTTGCCGCAGAGACAAAGAAGCAGCCCACTGTGACTCTTCTT 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 481 BP; 204 A; 82 C; 48 G; 145 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 57019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 10980; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monahan JE;
                                                                                                                                                                                                                                                                             ABV57028 standard; cDNA; 481 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0183319P.
2000US-0189862P.
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                          soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
     ccccccccccccccadartrariaritaaccccccritraaaagaaaaaaaaaaa
                                        ACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCC
                                                                                                               ACCAACAGAGCCTAAAAAAGACAAAAAAAAAAAAGACTGATGAAGCTCAGCCTTTGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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3.4%; Score 39; DB 12; Length 5284;
Best Local Similarity 54.4%; Pred. No. 1.7;
Matches 98; Conservative 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Human soft tissue sarcoma-upregulated DNA - SEQ ID 7691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 7691; 210pp; English.
                                                                                                                                                                                   769 GAGACAAAGAAGCAGCCCAC 789
                                                                                                                                                                                                                     187 AAAAAAAAAGGCCCCCCCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                             ADQ24871 standard; DNA; 5284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-2003; 2003WO-US038193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004048938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                 ADQ24871;
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                                                                                                               709
                                            649
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565 GTCTACACATGGAGAATAATANCTAGTTGACAAAAGCCANTTTAAGCAAGACATCTGCAA 624

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This invention relates to novel mammalian genes involved in viral infection and tumour suppression. Specifically, it refers to methods for infection and tumour suppression. Specifically, it refers to methods for identifying cellular genes that are required for viral, bacterial or parasitic growth, as well as genes used for tumour progression, but that are not essential for cell survival. The present invention describes a 'gene trap' method and screening/ selection process that can isolate of those polynucleotides that are associated with a specific process of interest. Furthermore, this method relies on the core discovery that virally infected cells become dependent on a serum survival factor that cover and after non-infected cells. Accordingly, identification of these factors and the appropriate inhibitors thereof, provides a means to treat and or prevent viral, bacterial or parasitic growth and infection, as well as tumour growth. The compositions of this invention exhibit cytostatic, virucidal, antibacterial and antiparasitic activities. This polynucleotide is a rat cDNA sequence that is necessary for viral infection, given in an exemplification of the invention.
                                                                                                                                 5210
                                                                                                                                                                                                                         5211 ATCATCTGATAAGCACTTATGAGCCNCTGCCATGTTTAATAAAACTTGACAACTACAAAA 5270
                                                                                                                                                                              843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel gene useful for preparing a composition for reducing or inhibiting viral infection or for suppressing a malignant phenotype in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; viral infection; tumour suppression; bacterial; parasitic growth; gene trap; serum survival factor; cytostatic; virucidal; antibacterial;
665 GTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGG-CCTAA
                                          5091 GTGACACTTTGGAGCAAAAACCTTGCAGTGGTAAATAAAAAATTTCCAACAGGGAAAAAA
                                                                                                                             5151 AAAAAAAAAAAAAAAAAAAAGTTTTACCTAATATTTTGGCATATAAAATGCAGAAGAA
                                                                                                                                                                              784 GCCCACTGTGACTCTTCCTTCCTGCGCTGACATGGATGATTTCTCCAGACAACTTCAAAA
                                                                                       724 AAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGAAAAAGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 982;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.4%; Score 38.8; DB 12; Length 9.
Best Local Similarity 48.2%; Pred. No. 0.88;
Matches 94; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat cDNA sequence required for viral infection SeqID 289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 289; 662pp; English.
                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                       ADJ74375 standard; cDNA; 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2003; 2003WO-US013743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2002; 2002US-0377136P
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-143721/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiparasitic; rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004010925-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2004
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                                                                                                                                                                                                                                                                                           RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AAAGTITCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCT 373
                  625 ICCTCANCANCATGACATTGACTTTAAATCACAGCCAANGGACAACACTCCTAAANTTC 684
                                                                                        853 MWWRYTMYTYCYAMTCAKCKYKMAMTKWWTTMACAWRATSWRWRAMAGMRWKRYKMKRAY 794
                                                            Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
610 ACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGGAGCCTAAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; rice;
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3.4%; Score 38.6; DB 8; Length 20
Best Local Similarity 10.2%; Pred. No. 1.4;
Matches 67; Conservative 299; Mismatches 278; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SA, Hou
Zhu T,
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e Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                          ADA71938 standard; DNA; 2000 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cooper B
                                                                                                                                                                                                                                                                                                        (first entry)
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illustrate the invention.
                                                                                                                                                      745 ATTGGGTTTTTTCC
                                                                                                                               790 TGTGACTCTTCTTCC
                                                                                                                                                                                                                                                                                                                                      Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang H, Chen W, Co
Katagiri F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression
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610 GACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCAT 669

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                                         613 MSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYK 614
                                                                                                                                             613 SMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRWSGMSRMYMKWMKKMRKRKYMRYMKWK 554
                                                                                                                                                                              CTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTCAAAGACAACGTCATAC 671
                                                                                                                                                                                           672 TGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGACA 731
                                                                                                                                                                                                                                       38 SMKYG----AKGCYGCKMMTYCSYGYMKWYTYMGSYKYSRCYKYMRMYMYKGWMYMMYYS 383
                                                                                                                                                                                                                                                                                                                                382 AYSSMMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWWCYMKCMRCYRWRKMMRKKT 323
                                                                                                                                                                                                                                                                                                                                                              374 GAGGCATCTAAAAAGCCTCGCCAAAAAGGTACTGCCACAAAACAGTACAAGGTCACTCAA 433
                   734
                                                                                    TCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCCACAATTTGCTCCAAGTGCCT 551
                                                                                                                                  CTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCTTCGGGAACATGGCTGA 611
                                                                                                                                                                                                                                                                      792 TGACTCTTCTTCCTGCGGCTGACATGGATTTTCTCCAGACAACTTCAAAATTCCATGA 851
              KYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKMYKKWW
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Search completed: May 15, 2005, 11:25:14 Job time : 719.805 secs

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NAME/KEY: promoter
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2817, Ap
967, App
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                                                                                                                          May 15, 2005, 11:11:51 ; Search time 249.39 Seconds (without alignments) 7453.434 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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Compugen Ltd.
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US-09-248-796A-5056
US-08-232-463-14
US-09-949-016-15911
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US-09-949-016-1742
US-09-949-016-1782
US-09-949-016-1782
US-09-949-016-1782
US-09-949-016-1056
US-09-949-016-105714
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               GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                         nucleic search, using sw model
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Match
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LOCATION: [1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
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                                                91446, A
11925, A
14368, A
14513, A
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; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR PLING DATE: 1999-08-04
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PATENTIN VERSION 3.0
; SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCCTGCGGCTGACATGGATGTTTCTCCAGACAACTTCAAAATTCCATGAGTGGAGC
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11.7%; Pred. No. 0.0059;
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Best Local Similarity 11.7%; Fred. No. 0.0059;
Matches 36; Conservative 142; Mismatches 130; Indels
US-09-710-279-3544
US-09-107-433-269
US-09-383-110-2008
US-08-961-527-275
US-09-949-016-11925
US-09-949-016-11925
US-09-949-016-11925
US-09-949-016-114368
US-09-349-016-114513
US-09-332-616A-224
US-09-352-616A-224
US-09-159-812-224
US-09-688-166A-224
US-09-688-166A-224
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US-09-689-166A-224
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ORGANISM: Artificial sequence
  1038 CAATGTGTA 1046
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Sequence 15911, Application US/09949016

Sequence 15911, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOD1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 AACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTCGGGGAC 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.4%; Score 38.6; DB 1; Length 7. Best Local Similarity 3.9%; Pred. No. 0.46; Matches 14; Conservative 195; Mismatches 154; Indels
                    NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REGISTRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear inmediate inmediate inmediate source: CLONE: pTZgpt-F1s US-08-232-463-14
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LENGTH: 13489
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                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5056
LENGTH: 2889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1674 TCGAGATATTACAGTGGATGAAAACAATCAACCCTCCAAAAAACACAAAAAGGAACCGAC 1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
APPLICANT: 520ENCES: 52
CONRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: VA
ZIP: Z2313-0299
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
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CLASSIFICATION: 435
RICR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                        Sequence 5056, Application US/09248796A
Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5670367
GENERAL INFORMATION:
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US-09-248-796A-5056
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     151 AAWTNNKTA 143
                                                                                                   US-09-248-796A-5056
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652 ATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACC
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                                                                                                                                                                                                                                                                                                Score 36; DB 4; Length 110402;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                          0; Mismatches 110;
                 PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                           3.2%;
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Best Local Similarity 50.49
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                          Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-12741/c
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                      US-09-949-016-17295
                                                                                                                                                                     SEQ ID NO 17295
LENGTH: 110402
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LENGTH: 110403
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLTMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
REALOR PEPLICANTION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                11661 GGAAGTAACACGTCTGGCACCAGAGTTGTTTAATTTGTCCTAAAGCCGCTGAAGCAA 11602
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                                                                                                                                               583 GGAAGTCACACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAA 642
                                                                                                                                                                                                                              643 AGATCCACAATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAAC 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 AAAGGCCAACAACAACAAGCCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386 AAGCCTCGCCAAAAACGTACTGCCACAAACAGTACAACGTCACTCAAGCATTTGGGGAGA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AAGAGTCAATACCCACTGAAGCCACCATTCACGCAGGAGACAACAAAAGAACCTCCAAC 63
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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0
                                                           Score 37.4; DB 4; Length 13489;
Pred. No. 1.6;
0; Mismatches 76; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                           ATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 4
Pred. No. 0.7;
0; Mismatches
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; Sequence 17295, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 53337, Application US/09949016
Patent No. 6812339
                                                           3.3%;
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Best Local Similarity 54.5%;
Matches 72; Conservative
                                                                                 Best Local Similarity 52.29
Matches 83, Conservative
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, ORGANISM: Human
US-09-949-016-15911
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LENGTH: 601
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; Sequence 12741, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOOU3307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTMARE: PESESEQ for Windows Version 4.0
                                                                                                                               16339 AGAGAACCCTAATACAATCATACACAAAATTTCTTAACCCAAAAAGTGTTTAGTGAAGAA 16280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16406 ATATATATATATACACATATATACACACACACATCTATCCTATTAATTCTCCCTCT 16347
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                                                                                 772 ACAAAAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGTTTCTCCAG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652 ATTCAAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACC 711
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Pred. No. 16;
0; Mismatches 110; Indels
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CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                        Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1058, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Dt FL genes Version 1.0 SEQ ID NO 1058
                                                                                                                           ) OTHER INFORMATION: n = A,T,C or US-09-949-016-13280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) LOCATION: (1)...(1450)
) OTHER INFORMATION: n = a,t,c or US-09-620-312D-1058
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5%;
Matches 72; Conservative
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Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wang, Dunrui
Wang, Zhiwei
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ORGANISM: Homo sapiens
                                                                                              FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
  SEQ ID NO 13280
LENGTH: 139952
TYPE: DNA
ORGANISM: Human
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Sequence 13280, Application US/09949016
Sequence 13280, Application US/09949016
Sequence 13280, Application US/09949016
Sequence 13280, Application US/09949016
SEREAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABELSEQ for Windows Version 4.0
                                                                                                                                                                                                                            Sequence 11782, Application US/09949016

Sequence 11782, Application US/09949016

Sequence 11782, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0
73821 AAGCAAGGCACTGAAAGTACTGAATCAAAACTTAAAGCACTCACACGAGGAAAGGAAAA 73762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73881 AAGAGTCAÁTACCCACCACCACCATTCACGCAGGAGACAACAAAGAACCCTCCAAC 73822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 AAAGGCCAACAACAACAAGCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCATCTAAA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 AAGCCTCGCCAAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGA
                                                                                                   16228 AGGTAGTTATTTTCAGGAGTGGATCAGCTGCAGACCTAAGCTAG 16183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%; Score 36; DB 4; Length 139936; Best Local Similarity 54.5%; Pred. No. 18; Matches 72; Conservative 0; Mismatches 60; Indels 0
                                                                          832 ACAACTICAAAATICCAIGAGIGGAGCTICIGCIGAITCAACTCAG 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;

LOCATION: (1)...(139936);

CTHER INFORMATION: n = A,T,C or G

US-09-949-016-11782
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US-09-949-016-11782/c
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LENGTH: 139936
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326 AAAGGCCAACAACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGAGGCATCTAAA 385
                                                                                                                                                      386 AAGCCTCGCCAAAAACGTACTGCCACAAAACAGTACAACGTCACTCAAGCATTTGGGAGA
                                       Gaps
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DB 4; Length 139952;
18;
                                       Indels
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APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP28
                                       90;
                                   0; Mismatches
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TYPE: DNA 'ORGANISM: Human
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                               196 TICAAGAAATICAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTGGAATGGCTAGCGG 255
                                                                                                                     196 TTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCTCCTGCTCGAATGGCTAGCGG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          693 TTCGAGAAAATCAACTTCTTGCACAAGAAGCAGAATTCTTTCAGCTCAAGGGACTGGCAG 752
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  Score 35.8; DB 4; Length 1450;
Pred. No. 1.4;
0; Mismatches 22; Indels 0
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                                                                                                                                                                                                                                                                                                                                                       SCHERANT INFOCRATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Watch
APPLICANT: Watch
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761e1 Human Potassium Channels
FILE REPERENCE: SEQ-159
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/106,687
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 87
SOFFWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 1.6;
0; Mismatches 22;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09336643A Patent No. 6399761 GENERAL INFORMATION:
Query Match 3.2%;
Best Local Similarity 69.0%;
Matches 49; Conservative
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Best Local Similarity 69.0%;
Matches 49; Conservative (
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LOCATION: (383)...(1157)

CTHER INFORMATION: K+Hnov15

US-09-336-643A-11
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753 AGGAAGTGAAA 763
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LENGTH: 1862
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Pred. No. 1.7;
0; Mismatches 62;
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53338
LENGTH: 601
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US-09-949-016-102714
; Sequence 102714, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 53.77
Matches 72; Conservative
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APPLICATION TO Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 102714

LENGTH: 601
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APPLICANT: Iandolo, John J.
APPLICANT: Crupper, Scott S.
TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.1%; Score 34.8; DB 4; Length 601; Best Local Similarity 53.7%; Pred. No. 1.7; Matches 72; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REGISCHOCKET NUMBER: 25043-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEPRAX: 816/474-9057
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Patent No. 6043219
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ORGANISM: Human
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                                                                                                                                                                                                                                 Score 34.8; DB 3; Length 6755; Pred. No. 7.2; 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 15, 2005, 14:22:59 Job time: 253.39 secs
                                                                                                                                           STRAIN: Graphylococcus aureus; STRAIN: UT0007
                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                      3.1%;
INFORMATION FOR SEQ ID NO: «
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.9°
Matches 66; Conservative
                                                  nucleic acid_
EDNESS: double
                                                                                   unknown
                                                  TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: unkn
                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
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May 15, 2005, 12:53:36 ; Search time 838.5 Seconds (without alignments) 8291.679 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                          1 aggcatcgtatgggttgcaa......tgaataatgctagggagagc 1136
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-699-936-16
US-10-889-447-3
US-10-889-447-6
US-10-889-447-6
US-10-827-757-1
US-10-829-936-1
US-10-839-936-1
US-10-839-729-17
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Maximum Match 100%
Listing first 45 summaries
                                                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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No.
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Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 1836, Ap
Sequence 30203, A
Sequence 30203, A
Sequence 30203, A
Sequence 30204, A
Sequence 112, Appli
Sequence 30203, A
Sequence 30203, A
Sequence 112, Appli
Sequence 57047, Appli
Sequence 7691, Appli
Sequence 7691, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74109, A
Sequence 252, App
Sequence 1541, Ap
Sequence 6128, Ap
Sequence 89737, A
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US-10-809-447-110

US-10-809-447-110

US-10-809-447-110

US-10-809-447-110

US-10-809-447-110

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US-10-809-447-110

US-10-809-447-110

US-10-699-936-1110

US-10-699-936-1110

US-10-313-345A-30204

US-10-363-345A-30204

US-10-363-345A-30204

US-10-363-345A-30204

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US-10-723-860-7691
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## ALIGNMENTS

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Sequence 1, Application US/10764075;
Sequence 1, Application US/10764075;
Publication No. US20040265796A1
GENERAL INFORMATION:
APPLICANT: Briese, Thomas
APPLICANT: Lipkin, Ian W.
APPLICANT: Palacios, Gustavo
APPLICANT: Jabbado, Omar
TILE REFERENCE: 5199-87
CURRENT APPLICATION: Methods and Kits for Detecting SARS-Associated Coronavirus
FILE REFERENCE: 5199-87
CURRENT APPLICATION NUMBER: US/10/764,075
CURRENT APPLICATION NUMBER: Provisional Application 60/463,704
PRIOR FILING DATE: 2003-04-17
NUMBER OF SEQ ID NOS: 16
SEQ ID NOS: 16
SEQ ID NO 1
CURRENT APPLICATION VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic nucleic acid sequence that includes the 3' OTHER INFORMATION: region of the SARS-associated coronavirus genome and OTHER INFORMATION: the N gene of the SARS-associated coronavirus genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1136;
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Pred. No. 0;
; Mismatches
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Best Local Similarity 100.0%; Pr
Matches 1136; Conservative 0;
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US-10-699-936-16
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gillim-Rose, Laura
APPLICANT: Gillim-Rose, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT PILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARR: PatentIn version 3.2
SERVINGTH: 1620

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Publication No. US20050075307A1;
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ray;
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
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1541 TCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAGC 1596
                                                                                                       GCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGTTCTCCAGACAACTTCA
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Publication No. US205007530741

GENERAL INFORMATION:

APPLICANT: Jain, Ravi

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

TITLE OF INVENTION NUMBER: US/10/889,447

CURRENT APPLICATION NUMBER: 05/46,670

PRIOR FILING DATE: 2004-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: PSELSEQ for Windows Version 4.0

LENGTH: 24774
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; Sequence 10 VS20050075307A1
; GENERAL INFORMATION 10 VS20050075307A1
; APPLICANT: Bennett, C. Frank
; APPLICANT: Bannett, C. Frank
; TILE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 1136; Conservative
   GCAGCCCACTGTGACT
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FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
FRIOR PILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOCTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 28920
TYPE: DNA
TYPE: DNA
PEATURE: SARS COFONAVITUS isolate BJ03
FEATURE: NAMEXEY: misc_feature
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Matches 1136; Conservative
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                             TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-15
                                                                                           Query Match 100.
Best Local Similarity 100.
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SEQ ID NO 15
LENGTH: 29727
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TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK.0134
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR PILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FRRENCE OF WINDOWS VERSION 4.0
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Publication No. US20050002953A1
GENERAL INFORMATION:
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; Publication No. US20050075307A1
; GENERAL INFORMATION:
    APPLICANT: Bennett, C. Frank
    APPLICANT: Bennett, C. Frank
    TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
    TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
    CURRENT APPLICATION WUMBER: US/10/889,447
    CURRENT PILING DATE: 2004-07-12
    PRIOR APPLICATION NUMBER: 60/486,670
    PRIOR FILING DATE: 2003-07-12
    NUMBER OF SEQ ID NOS: 241
    WUMBER OF SEQ ID NOS: 241
    SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 0;
iive 0; Mismatches
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US-10-889-447-8
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Sequence 1, Application US/10827757

Publication No. US20050004071A1

GENERAL INFORMATION:

APPLICANT: Comper, Wayne

TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During TITLE OF INVENTION: Ridney Filtration And Renal Passage And Their Use To Treat Or TITLE OF INVENTION: Prevent Infection By Coronaviruses

TITLE OF INVENTION: Prevent Infection By Coronaviruses

CURRENT APPLICATION NUMBER: US/10/827,757

CURRENT APPLICATION NUMBER: 60/464,294

PRIOR FILING DATE: 2003-04-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.2

SEQ ID NO 1
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100.0%; Score 1136;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches
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                      Sequence 1, Application US/1069936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Gabol, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1136; Best Local Similarity 100.0%; Pred. No. 0; Matches 1136; Conservative 0; Mismatches
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dain, Ravi
TITLE OF INVENTION: MODILATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0665US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PILING DATE: 2003-07-12
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US-10-889-447-9
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Sequence 17, Application US/10839729
Publication No. US2005002953A1
GENERAL INFORMATION:
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT APPLICATION NUMBER: 60/468703
PRIOR PILING DATE: 2004-05-04
PRIOR RILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FSELSE (or Windows Version 4.0)
SEQ ID NO 17
LENGTH: 29736
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US-10-839-729-17
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ive 0; Mismatches
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Matches 1136; Conservative
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Windows Version 4.0
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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LENGTH: 29736
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                                              TYPE: DNA ORGANISM:
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Sequence 3, Application US/10699936;
Sequence 3, Application US/10699936;
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory;
TITLE OF INVENTION: Syndrome Coronavirus
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                             CCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCGAAATTGCACAATTTGC
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Publication No. US20050002953A1
GENERAL INPORMATION:
APPLICANT: Jens Herold
ITILE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR RPLICATION NUMBER: 60/468703
PRIOR RPLICATION NUMBER: 2003-06-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 29742
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Pred. No. 0;
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100.0%;
Best Local Similarity 100.0%;
Matches 1136; Conservative 0
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       GAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAACAGTA
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APPLICANT: PETRIS, JOSEPH S. M.

APPLICANT: PETRIS, JOSEPH S. M.

APPLICANT: PETRIS, LIT MAN

APPLICANT: PETRIS, LIT MAN

APPLICANT: TGNA, VII MAN

APPLICANT: GTNA, VII MAN

APPLICANT: GTNA, VII MAN

APPLICANT: MUNCHOLLS, JOHN

ITILE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)

CURRENT FILING DATE: 2004-03-24

PRIOR FILING DATE: 2003-04-02

PRIOR PLICATION NUMBER: 60/457, 730

PRIOR APPLICATION NUMBER: 60/459, 931

PRIOR APPLICATION NUMBER: 60/459, 931

PRIOR APPLICATION NUMBER: 60/469, 931

PRIOR APPLICATION NUMBER: 60/469, 935

PRIOR APPLICATION NUMBER: 60/469, 935

PRIOR APPLICATION NUMBER: 60/469, 935

PRIOR PLING DATE: 2003-04-04

PRIOR PLING DATE: 2003-04-14

PRIOR PLING DATE: 200
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100.0%; Score 1136;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1136; Conservative 0; Mismatches
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ORGANISM: Human severe acute respiratory system virus
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100.0%; Pred. No. 0;
ative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR FILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR PILING DATE: 2003-04-08
PRIOR PILING DATE: 2003-04-14
PRIOR PILING DATE: 2003-04-05
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: PETENTIN VOY: 3.2
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NAME/KEY: CDS

; LOCATION: (1)..(29742)

US-10-808-187-16
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Best Local Similarity
Matches 1136; Conserv
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Targe-scale identification of ESTs involved in the interaction Unpublished (2003)
Contact: Rod Wing
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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OSJNE601G10.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
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/organism="Oryza sativa (japonica cultivar-group)"
                 AK032314 A
AK083404 BJ38780 AZJ38780 AZG477863 AZG477863 AZG477863 AZG77863 AZG778714 AZG6784 BF286190 BF566518 G
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
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Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
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BF598760 8v21d10.y
BJ362480 BJ362480
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BJ39757 BJ386277
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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BJ328127 Bictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda23e04 5', mRNA sequence.
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                                                       253 AAAGCCAGTAGAAACTGNNTCAATAAAAGAGCAAAAAAAATGCAACAACAATAAGACAC 194
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1 (Dases 1 to 640)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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/clone_lib="Dictyostelium discoideum cDNA library, AF"
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/organism="Dictyostelium discoideum"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.8%; Score 42.8; DB 4;
48.2%; Pred. No. 0.68;
iive 0; Mismatches 128;
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Location/Qualifiers
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/strain="AX4"
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Dictyostelium discoideum
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Sorghum bicolor
Sorghum bicolor
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
(blase 1 to 333)
Wyrich,R., Dressen,U., Brockmann,S., Streubel,M., Chang,C.,
Qiang,D., Paterson,A.H. and Westhoff,P.
The molecular basis of C4 photosynthesis in sorghum: isolation,
bundle-sheath-specific cDNAs obtained by differential screening
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HHU58b Sorghum bicolor cv. TX430 Sorghum bicolor cDNA clone HHU58
'similar to transketolase, chloroplast (TKLC1), mRNA sequence.
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Contact: Westhoff P
Plant Molecular Biology
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/strain="cv. TX430"
/db xref="taxon:4558"
/clone="HHU58"
/clone=lHHU58"
/clone=lhb="Sorghum bicolor cv. TX430"
/note="Vector: Lambda ZAP II; leaf cDNA library,
unidirectionally cloned"
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Universitaetsstrassel, D-40225 Duesseldorf,
Tel: (49)-211-311-338
Fax: (49)-211-311-4871
Enail: west@uni-duesseldorf.de
Homology: sp/p22976, Blastx-Score: 176, pVal
Seq primer: M13 (-20).
               2;
0.55;
         DB 6;
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         Score 43.2;
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Best Local Similarity 52.6%;
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         3.8%;
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531

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EST 07-MAR-2002
Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 AACAAAACAGGTGGTAACAAATGATTTTGGATTACTTGGACCTGCATTTACACCAGTTAA 330
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Glycine soja
Glycine soja
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 caaatriigcaccagrigaagrgaaatcatriiggaatracaaacrcaarrciaacrggga 210
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                                                                                                                                                                                                                                                             Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

    (bases 1 to 434)
    Urushihara, H. Tanaka, Y., Kohara, Y. and Shin-i, T.
    Full length cDNA of Dictyostelium discoideum at the culmination

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCCACA
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                                                                         BJ358542 Bictyostelium discoideum cDNA library, CF discoideum cDNA clone ddc10f01 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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/clone="ddc10f01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovy Osocgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699 AAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAGC 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    870 CMTMC-CCMMMMANAMAHWHACHWHWAHAWTHMCMCCCCCTMMMHAHTWWHHHH 928
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AL068607
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                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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18.7%; Pred. No. 1.1;
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                                                                                                                       Drosophila melanogaster (fruit fly)
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/db_xref="taxon:7227"
/clone="back32023"
/clone_lib="RPCI-98"
/note="end : TET3"
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                                                                         AL068607.1 GI:4958689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /done lib="Gm-c1057"
//once="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//once="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//once="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//once="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//once="Vector: pBluescript II SK+; Site 1: EcoRI alone
//once degenerating cotyledons of 2 week old seedlings from
//once for for from the strong from mRNA
//once for for from mRNA
//once for 
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                          Glycine.

1 (bases 1 to 518)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is liseted in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423, 4163; email: info@biogeneticservices.com)
High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 agcaagcaarriagrgacacacaaagaracagaragraaaacrraaccarcracrgcaaaacga 273
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eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 GCCAATCTAGAAGCTCCCATCCTTTTGAACAAGGGATCCTTGACACGCAAAAGCGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine soja"
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/mol_type="maNA"
/mol_type="taxon:348"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1057-187"
/tissue_type="Degenerating cotyledons, 2 week old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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Pred. No. 0.96;
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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BJ362480/c
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JOURNAL
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KEYWORDS
SOURCE
                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 acchegnneraaaccacheaaneacearcrarcarriteaarceerieraaceerrecaaa 288
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1 (bases 1 to 556)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
I (bases 1 to 540)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Culmination stage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 AACAAAACAGGTGGTAACAAATGATTTTGGATTACTTGGACCTGCATTTACACCAGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                  Tall Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Contact: Tadasu Shin-i
Contert: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.7%; Score 42.2; DB 4; Similarity 48.2%; Pred. No. 0.97; Conservative 0; Mismatches 128;
                                                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:44689"
/clone="ddc22a02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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BJ366773.1 GI:19276075
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                                                                                                                                                                                         Unpublished (2002)
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BJ339144 Incay 601 bp mRNA linear EST 07-MAR-2002 BJ339144 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda64f10 5', mRNA sequence.
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                                                                                                                        303 AACAAAACAGGTGGTAACAATGATTTTGGATTACTTGGACCTGCATTTACACCAGTTAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s82 aacaaaacaggregraacaaargarririggarracriggaccrecarrracaccagrraa 523
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                                                                                                                                                                                                           243 AGATTTTGGAATCAAACCAATGCTTAAGTCAATAGATTGACCAACTGTTACGAAATTTAC 184
                                                                                                                                                                                                                                                       532 ACAATTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCAC 591
                                                                                                                                                                                                                                                                                              183 caaaririgcaccagrigaagrgaaarcarrrggaarracaaacccaarrcraacrgggaa 124
                                                                                                                                                                                                                                                                                                                                        592 ACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACA 651
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1 (bases 1 to 601)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="mat A"
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/clone_lib="Dictyostelium discoideum cDNA library, AF"
                                                                                     412 AAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACCAAAACCCAAGGAAA
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      Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
  3.7%; Score 42.2; DB 4;
48.2%; Pred. No. 1;
tive 0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="dda64f10"
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Dictyostelium discoideum
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                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           652 ATTCAAA 658
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                        Best Local Similarity
Matches 119; Conserv
    Query Match
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ORGANISM
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                                             1. .556
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dc40004"
/sex="mat A"
/dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
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1 (bases 1 to 593)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Pull length cDNA of Dictyostellum discoideum at the aggregation
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/clone="dda28e11"
/sex="mat A"
/dev stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Center For Genetic Resource Information
National Institute of Genetics
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .556
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Location/Qualifiers
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/strain="AX4"
/db xref="taxon:44
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                  403
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                                                                        ACCTGGTTGTAAACCACTGAATGACCATCTACCATTTGAATCGGTTGTAACGGTTCCAAA 343
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1.0 605)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
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389 caaatiticcaccagridaagrgaaatcartificaartracaaactcaartcraactggaa
                                               ACCTTCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACA
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|mol_type="mRNA"
|strain="AX4"
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Pred. No. 1;
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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/clone="ddc35m13"
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Location/Qualifiers
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Best Local Similarity 48.23
Matches 119; Conservative
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BJ339537 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda65017 5', mRNA sequence.
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1 (bases 1 to 606)

1 Urushihara,H. Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (basea 1 to 616)
Urushihara 1 to 7 Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the slug stage
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3.7%; Score 42.2; DB 4; Length 6
Best Local Similarity 48.2%; Pred. No. 1;
Matches 119; Conservative 0; Mismatches 128; Indels
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/mol_type="mRNA"
/strain="AX4"
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Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                Dictyostelium discoideum
Dictyostelium discoideum
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BJ387757.1 GI:19297141
                                                                                                        BJ339537.1 GI:19247899
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BJ370135 Bctyostelium discoideum cDNA linear EST 08-MAR-2002 BJ370135 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA clone ddc53d06 5', mRNA sequence.
                                                                                                                                                                                                                                             412 AAAACAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAAGGAAA 471
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1 (bases 1 to 629)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
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48.2%; Pred. No. 1;
tive 0; Mismatches 128; Indels
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Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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48.2%; Pred. No. 1;
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1 (bases 1 to 617)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the culmination
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         Contact: Tadaeu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
1811 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes nig.ac.jp.
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Nata, Mishima, Shizuoka 411-8540, Japan
Tal: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Db 571 AACAAACAGGTGGTAACAGATTTTGGATTATTGGATTTTGCATTTTACACCAGTTTAC 512

Qy 472 TTTCGGGACCAAGACCTAATCAGATAGATTACAACATTTGCCGCAAATTGC 531

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Qy 652 ATTCAAA 658

Db 331 GAGGAA 325

Search completed: May 15, 2005, 14:18:37

Job time: 5008.54 sec8
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SARS coronavirus BJ01 nucleocapsid protein mRNA, complete cds.
AYS36760
                               coro
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Coronaviridae; Coronavirus.
Lit., Lit., Liu. and Chang, Z.

Light. Lit., Liu. b.

Light. Beijing, Beijing 100084, China

Light. Lit., Lit. b.

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Light. Lit., Lit. b.

Light. Beijing, Beijing 100084, China

Light. Lit., Lin. and Chang, Z.

Light. Light. Beijing, Beijing 100084, China

Sequence update by submitter

Light. Lit., Lit., Chang, Z. and Liu. L.

Light. Lit., Lit., Chang, Z. and Liu. L.

Light. Lit., Lit., Chang, Z. and Liu. L.
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AY348314
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Li,T., Li,X., Chang,Z. and Liu,L.
Identification of SARS-COV mRNA leader sequence
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May 15, 2005, 11:00:45 ; Search time 95.9067 Seconds (without alignments) 10609.895 Million cell updates/sec
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Copyright (c) 1993 - 2005
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9b htg: *
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/translation="MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV
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db_xref="GI:32454349"
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/product="Orf7b"
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Best Local Similarity 100.0%; P:
Matches 21; Conservative 0;
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AY322205S4
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RACALLLLDRANDLESKVSGKGQQQQQTVTKKSAABASKKRKPQKRTATKQNVTYQAFG
RRCALGOGGRING IRQCTYKHWPQ1AQPAPSASAPFGMSR1GMSVTPGSCTMLTY
HGA1KLDDKOPFONVILLINGHIDAVKTFPPTEPKKONKKKTDBAQPLPQRQXKQPT
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Li (bases 1 to 1873)

Lim, P.L., Kurup, A., Gopalakrishna, G., Chan, K.P., Wong, C.W., Ng, L.C., Se-Thop, A., Gopalakrishna, G., Chan, K.P., Wong, C.W., Miller, L.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B. and Leo, Y.S.

Laboratory-acquired severe acute respiratory, syndrome (SARS) - Singapore 2003

Unpublished
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Pred. No. 0.62;
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SARS coronavirus Sin_WNV, partial sequence.
AYS34767
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SARS coronavirus Sin0409, partial sequence.
AY534761
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                                                                                                                                                                         VTPLPAADMDDFSRQLQNSMSGASADSTQA"
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100.0%; Pred. No. v..
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SARS coronavirus Sin0409
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Best Local Similarity
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AY534762S6
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AY534758S4
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VERSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis Street, 02-01, Genome, Singapore 138672, Singapore Location/Qualifiers
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Yuan, Z., Zhang, X., Hu, Y., Lan, S., Wang, H., Zhou, Z. and Wen, Y.
Direct Submission
Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical
College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032,
P.R. China
SARS coronavirus Sin WNV
SARS coronavirus Sin WNV
Viruses, ssRNA positive-strand viruses, no DNA stage; Nidovirales,
Coronaviridae; Coronavirus.

1 (bases 1 to 1938)
Lim, P.L., Kurup, A., Gopalakrishna, G., Chan, K.P., Wong, C.W.,
Ng, L.C., Se-Thoe, S.Y., Oon, L., Bai, X., Stanton, L.W., Ruan, Y.,
Miller, L.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J.,
Miller, L.D., vega, V.B., accute respiratory syndrome (SARS) -
Singapore 2003
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                                                                                                                                                                                                                                                                                                Singapore 2003
Unpublished
2 (bases 1 to 1938)
Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY322205S4 2304 bp RNA linear VRL 21-JUL-2 SARS coronavirus Shanhgai LY Orf7a gene, partial cds; and Orf7b, Orf8A, Orf8b, and nucleocapsid protein genes, complete cds. AX322208
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Pred. No. 0.62;
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17 Laozheda Rd., Hangzhou,
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of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou, Zhejiang 310009, China (Debises 1 to 2810)
Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L.
Direct Submission
Submitted (05-DEC-2003) Department of Microbiology, Zhejiang of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou, Zhejiang 310009, China
Nucleotide and amino acid sequences updated by submitter On Dec 5, 2003 this sequence version replaced gi:31505969.
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Mote="transcription regulatory core sequence
162. .353
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protein id="AAR27476.1"
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QLPQGTTLPKGFYAEGSRGSQASSRSSRSRGNSRNSTPGSSRGNSPARMASGGGFT
ALALLLLDRLNQLESKYSGKGQQQQGGTYTKKSAAEASKKPRQKRTATKQYNVTQAFG
RRGPBQTGGNFGDQDLIRQGTDYKHWPQIAQPAPSASAFFGMSRIGMEAAPSGTWLTY
HGAIKLDDKDPQFRONVILLANKHIDAYKTPPPTEPKKDKKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA"
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Wang, Z.G., Li,L.J., Luo,Y., Zhang,J.Y., Wang,M.Y., Cheng,S.Y.,
Zhang,Y.J., Wang,X.M., Lu,Y.Y., Wu,N.P., Mei,L.L. and Wang,Z.X.
Molecular biological analysis of genotyping and phylogeny of severe
acute respiratory syndrome associated coronavirus
Chin. Med. J. 117 (1), 42-48 (2004)
                                                                                                                                                                                                                                            /protein_id="AAP82973.1"
| Ab xref="G1:32454351"
| translation="WOLKILVRYNRGNTYSTAWLCALGKVLPFHRWHTWVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAARBVLVVLNKRTN"
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Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L.
Direct Submission
Submitted (03-MAY-2003) Department of Microbiology, Zhejiang Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLPNNTASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKM
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Coronaviridae; Coronavirus.
1 (bases 1 to 2810)
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                                                                                               protein id="AAP82972.1"
/db_xref="GI:32454350"
/translation="MKLLIVLTCISLCSCICTVVQRCASNKPHVLEDPCKVQH"
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Pred. No. 0.63;
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/protein_id="AAP82974.1"
/db_xref="GI:32454352"
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product="Orf8A"
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/product="Orf8b"
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ilarity 100.0%;
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VRL 05-NOV-2003

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SARS coronavirus SZ13
SARS coronavirus SZ13
Viruses; seRNA postive-strand viruses, no DNA stage; Nidovirales;
Viruses; seRNA postive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 8581)
1 (bases 2 to 8581)
1 (bases 3 to 8581)
1 (bases 3 to 8581)
2 (ban, X. Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.P., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
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Guan, Y. and Zheng, B.J.
Direct Submission
Submission
Submitted (26-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
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SARS coronavirus GZ60
Viruses; sBRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAX-2003) Microbiology, The University of Hong Kong,
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Guan, Y., Zhang, I. to 11006)
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Dhan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
Isolation and characterization of viruses related to the SARS
Science 302 (5643), 276-278 (2003)
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/organism="SARS coronavirus SZ13"
/mol_type="genomic RNA"
/db_xref="KZ13"
/db_xref="texon:231514"
/country="Hong Kong"
                                                                                                            p RNA
genome.
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8268 ATGACCACACAGGCAGATGG 8288
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LLAAVGEIILLEWLAEVVKLPSRYCC"
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                                             ALALLLLDRLNQLESKVSGKGQQQGGTVTKKSAAEASKKPRQKRTATKQYNVTQAFG
KREBEQTGRGDQDLIRGYOTDYKHWPOLAQFAPSASAFFGMSRIGMEVTPSGTWLTY
HGAI KLIDKUDQFKNVVILLINKHIDAYKTFPPTBPKKDKKKKTDEAQFLPQRQXKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA"
                                                                                                                                                                                                                                             'tränslation="MDPNQTNVVPPALHLVDPQIQLTITRMEDAMGGGQNSADPKVYP"
IILRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK"
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SARS coronavirus SZ1
SARS coronavirus SZ1
Curuses; saRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 8439)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Lin, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.M.
Isolation and characterization of viruses related to the SARS
coronavirus from animals in southern China
Science 302 (5643), 276-278 (2003)
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1. .8439
//organismamsARS coronavirus S21"
//organismamsARS coronavirus S21"
//sol_type="genomic RNA"
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Pred. No. 0.63;
Mismatches 0; Indels 0
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                                                                                                                                                       /codon_start=1
/product="uncharacterized protein 9b"
/protein id="Adh6659.1"
/db_xref="GI:31747858"
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/country="Hong Kong"
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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Guan, Y. and Zheng, B.J.
Direct Submission
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VRL 05-NOV-2003

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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirdae; Coronavirus.

1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
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[ (bases 1 to 13471) Guan,Y., Zheng,B.J., He,Y.Q., Liu,X.L., Zhuang,Z.X., Cheung,C.L., Luo,S.W., Li,P.H., Zhang,L.J., Guan,Y.J., Butt,K.M., Wong,K.L., Chan,K.W., Lim,W., Shortridge,K.F., Yuen,K.Y., Peiris,J.S.M. and Poon,L.L.M.
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Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                         2 (bases 1 to 11010)
Guan,Y. and Zheng,B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
Location/Qualifiers
                                                                                                                                                        Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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/organism="SARS coronavirus HKU-66078"
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/country="Hong Kong"
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/isolate="GZ43"
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/isolate="HKU-66078"
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/country="Hong Kong"
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1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.

Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China
Science 302 (5643), 276-278 (2003)
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 11010)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-mAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
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Pred. No. 0.69;
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//mol type="ganomic RNA"
//solate="HKU-65806"
//db xref="HKU-65806"
//db xref="taxon:231220"
/country="Hong Kong"
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SARS coronavirus HKU-65806, partial genome.
AY304493
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                                                                        /organism="SARS coronavirus G260"
/mol type="genomic RNA"
isoIate="G260"
/db xref="texon:231518"
/country="Hong Kong"
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SARS coronavirus HKU-65806
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Matches 21, Conservative
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VRL 05-NOV-2003

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1 (bases 1 to 13471)

Guan, Y., Zheng, B.J., He, Y.O., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
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SARS coronavirus ShanghaiQXC2
Viruses; BSRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronavirdae; Coronavirus.

1 (bases 1 to 29013)
Yuan, Z., Zhang, X., Hu, Y., Lan, S.,, Zhou, Z., Wang, H. and Wen, Y.
Analysis of SARS coronavirus genome in Shanghai isolates
Uppublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 13471)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (2-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 29013)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.
Direct Submission
Submitted (11-NOV-2003) Key Lab of Medical Molecular Virology,
                                     Gaps
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SARS coronavirus ShanghaiQXC2, complete genome.
AY463060
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Pred. No. (
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/isolate="HKU-36871"
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/country="Hong Kong"
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Location/Qualifiers
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SARS coronavirus HKU-36871
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ENFSSRMYCSFYPPDEEEEDDAECEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVR
VEEEEEEDWLDDTTEQSEIEPEPTPEEPVNQFTGYLKLTDNVAIKCVDTVKEAQSA
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KPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNMLRGEDMSFLEEDAPYM
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ALKKCKSAFYVLPSEAPNAKEEILGTVSWNLREMLAHAEEARKLMPICMDVRAIMATI
QRKYKGVKIQBGIVDYGVRFFFYTSKEPVASIITKLNSLNEPLVTMPIGYVTHGFNLE
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GYRELGVERELKGDRKTVYHTLBSPVREHLDGEVLASLDKLKSLSLEREVKTIKVFTYVD
NYNLHTQLVDWSKYTGQQCGFTYLDGADYRKI KPHVNHEGKTFFVLBSDDTLASEAFE
YYHTLDESFLGRYMSALNHTKKWKFPQVGGLTSI KWADNNCYLSSVLLALQQLEVKFN
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VFYKETSYTTTIKPVSYKLDGVTYTEIEPKLDGYYKKDNAYVENTSITIKKPNELSLA
LGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCAKRLAQRVFNNYMPYVFT
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LLLLSICLGSLICVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTTMDFCEGSFFCSI
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AFFGYFASHFISNSWLMWFIISIVQMAPVSAMVRMYIFFRSFYYIWKSYVHIMDGCTS
STCMMCYKCNHATRVECTTIVNGMKRSFYVYANGGRGFCKTHNWNCLNCDTFCTGSTF
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NLDNILRANNTKGSLPINVIVPDGKSKCDESASKSASVYYSQLMCQPILLLDQALVSDV
GDSTEVSVKMFDAYVDTFSATFSVFMEKLKALVATAHSELAKGVALDGVLSTFVSAAR
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NVQLRVIGHSMONCLLRLKVDTSNPKTPKYKFVRIQPGQTFSVLACYNGSPSGVYQCA
MRPNHTIKGSFLNGSCGSVGFNIDYDCVSFCYMHHMELPTGVHAGTDLEGKFYGPFVD
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HVDIIGPLSAQTGIAVLDMCAALKELLQNGMNGRTILGSTILEDEFTPFDVVRQCSGV
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VVCKHCGQKTTTLTGVEAVMYMGTLSYDNLKTGVSIPCVCGRDATQYLVQQESSFVMM
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TLGVLVPHVGETPIAYRNVLLRKNGNKGAGGHSYGIDLKSYDLGDELGTDPIEDYSCON
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TTKISLKGGKIVSTCFKLMLKATLLCVLAALVCYIVMPVHTLSIHDGYTNEIIGYKAI
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                                                        200032, P.R. China
Location/Qualifiers
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FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFTLRNTVCTVCGMWKG YGCSCDQLREPLMQSADASTFFKRVCGVSAARLTPCGTGTSTDVVYRAFDIYNEKVAG FAKFLKTNCCRFQEKDEEGNLLDSYFVVKRHTMSNYQHEETIYNLIKDCPAVAVHDFF DWYDFVENPDILRVYANLGERVRQSLLKTVQFCDAMRDAGIVGYLTLDNQDLNGNWYD FGDFVQVAPGCGVPIVDSYYSLLMPILTLTRALAAESHMDADLAKPLIKWDLLKYDFT EERLCLFDRYFKYWDQTYHPNCINCLDDRCILHCANFNVLFSTVFPPTSFGPLVRKIF TTCFSVAALTNNVAFQTVKDGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAI SDYDYYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGCINANQVIVNNLDKSAGFPFNK WGKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYAISAKNRARTVAGVSICSTM TNRQFHQKLLKSIAATRGATVVIGTSKFYGGWHNMLKTVYSDVETPHLMGWDYPKCDR AMPNILRINAALVLARKGHTVCCNLSHFPRLABARGAQVLSEMYNGGGSTSYGROGTSS GDATTAYANSYFNICGQAYTANVNALLSTDGMKIADKYVRNLQHRLYSELYRNBDVDHF FVDEFYAYLRKHFSMMILSDDAVVCYNSNYAAQGLVASIKNFKAVLYYQNNVFMSEAK CWTETDLIKGPHEFCSQHTMLVKQGDDYVYLPYPDPSRILGAGCFVDDIVKTDGTLMI
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